

# STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 113237

TO: Robert Kelly Location: rem-2c55

**Art Unit: 1632** 

Search Notes

**February** <u>5</u>, 2004

Case Serial Number: 09971773

From: P. Sheppard

Location: Remsen Building

Phone: (571) 272-2529

sheppard@uspto.gov

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### STIC-Biotech/ChemLib

//3237

From:

Kelly, Robert

Sent:

Friday, January 30, 2004 6:03 PM

To:

∰STIC-Biotech/ChemLib

Subject:

09/971,773

With regard to Application No. 09/971,773, please run the following sequence searches:

Search for SEQ ID NOS: 1, 2, 23 and 24, with results of 80% or greater sequence homology

Also, search these same sequences allowing for at least 1 insertion, deletion, substitution, or addition

Thanks!

Robert M. Kelly, Ph.D. Room.2C55, Remsen Bldg. (571) 272-0729





Phone:	
Location:	
Date Picked Up:	
Date Completed:	_
Searcher Prep/Review:	-
Clerical:	
Online time:	
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Searcher:\_\_\_



TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:

Other:\_

VENDOR/COST (	(wnere applic.)
STN:	
DIALOG:	
Questel/Orbit:_	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	
WWW/Internet	:
Other (specify)	:

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model
Run on: February 2, 2004, 10:19:28; Search time 7369.83 Seconds (without alignments) 11146.322 Million cell updates/sec
Title: US-09-971-773-1 Perfect score: 2008 Sequence: 1 aacagaaacttatttcctggctgtgcctcaagcccatg 2008
Scoring table: IDENTITY NUC Gapop 10.0, Gapext 1.0
Searched: 2888711 segs, 20454813386 residues
Total number of hits satisfying chosen parameters: 5777422
Minimum DB seq length: 0 Maximum DB seq length: 200000000
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
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 1
2: gb_htg:*
8: gb_pl:* 9: gb_pr:*
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19: em_mu:*
22: em_ov:*
24: em_ph:* 25: em_pl:*
27: em_sts:*
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0 0
37: em_htg_vrt:*
40: em_htgo_mus:* 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		Query	;	į	;	
No	Score	Match	Length	88	QI .	Description
7	200	100.0	20	9	851	58516 Cell
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4	15	78.9		9	3517	58517
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9	575	78.4		σ	HSY17976	976 Ното ва
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80	575	78.4		σ	HSY17977	977 Ното вар
σ	575	78.4		σ	HSY17978 .	978 Homo
10	575	78.4		σ	HSY17979	979
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14	1575.2	78.4		σ	HSA536056	6
15	1572.8	78.3		9	E15725	10
16	1571.8	78.3		6	D89289	D89289 Homo sapien
17	1568	78.1		9	AR170077	Sequenc
18	514	75.4		9	AX662735	
19	1514.8	75.4		9	77	745
20	509	75.2		4	23	D86723 Porcine mRN
21	474	73.4		9	AR170074	374 Seguen
22	1474.2	73.4	1728	9	E14720	Pr
23	469	73.2		4	AF247186	AF247186 Bos tauru
24	256	62.6		6	BC025385	
25	1090.4	54.3		2	XLA514872	AJ514872 Xenopus 1
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27		48.6		9	BD168521	BD168521 Cells pro
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29	ω	43.9		9	E43925	E43925 Antibody re
30	. 60	40.3		6	AB049740	AB049740 Homo sapi
31	6	29.9			E43926	E43926 Antibody re
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## ALIGNMENTS

TCCTTGTGTGTACTTTT 1500 CTTACTTACCCTTGGCT 1020 CCAATTATGÀATTTATT 1380 |||||||||||||||| |CCAATTATGAATTTATT 1380 IGCATCCTGATGCCTCT 1560 AAGAGTGTATCTGGCC 1320 aggacaaaatgttcaa 960 |||||||||||||||| nggacaaaatgttcaa 960 GGACTGCAGCAAAGCC 720 STCAACTCCATGTG 780 PAGTGAGACATGCACA 900 AGAAGCCAAAGATCTG 660

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code: BCM-HGSC
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Best Local Similarity 94.1
Matches 1891; Conservative
                                                                                                     A.N., Gibbs, R.A.
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Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (bases 1 to 2976)

Strausherg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Sholler, G.D., Altschul, S.F., Zeeberg, B., Buetch, K.S., Schefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Staplecon, M., Soares, M.M. B., Bonddo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., McKernan, K.J., Mallahy, S.J., Boask, S.A., McKernan, P.J., Mallahy, S.J., Boask, S.A., McKernan, P.J., Wallahy, S.J., Garcia, A.M., Gay, L.J., Hulyk, S.W., Vilalon, D.K., Malah, J.M., Sodersten, P.H., Richards, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Buktenlied, N., Madan, A., Young, A.C., Shevchenko, Y., Buttersled, S.G., Blakesley, M. Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J.S., Schmutz, J., Myers, R.M., Generation and initial analysis of more than 15,000 full-length human and mouse odn. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Mus musculus fucosyltransferase 8, mRNA (cDNA clone MGC:11418
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Submitted (10-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                             GGAAAAACAGGCCTGTACCCTTCCTACAAAGTCCGAGAAGATAGAAACAGTCAAATAC
                                                                                                        CCTACATATCCTGAAGCTGAAAAATAGAGATGGAGTGTAAGAGATTAACAACAGAATTTA
                                                                                                                                               CCTACATATCCTGAAGCTGAAAATAGAGATGGAGTGTAAGAGATTAACAACAGAATTTA
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Tissue Procurement: Jeffrey Green M.D.
TONA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G. E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
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KEYWORDS
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AUTHORS
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AUTHORS
TITLE
JOURNAL
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/tissue type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse." /clone_libe:"NCI_CGAP_Mam6"
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KILAKLERLKQQNEDLRRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIENYKK
SARNGLGKDHÜTLRRRIENGAKELWFFLQSELKKLKKILEGBUELQRHADEILLDLGHHE
RSIMTDLYXLSQTDGAGDWREKEAKDLTELVQRRITQUPKDCSKARKLVCNINKG
GYGCQLHHVYÇCFMTAGTQRTLILESQNWRYATGGMETVFREVSETCTDRSGLSTGH
WSGEVUDKNIQVVELPIVDSLHPRPPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKY
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LARRMQVDKKQVYLATDDPTLLKEAKTKYSNYEFISDNSISWSAGLHNRYTENSLRGV
ILDIHFLSQANFLVCTFSSQVCRVAYEIMQTLHPDASANFHSLDDIYYFGGQNAHNQI
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                                                                                                                                                                                                              through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 16 Row! 1 Column: 5

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8393370.
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amgobcm.tmc.edu
Gunaratne, P.H., García, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowie, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               483 AAAAGAAACCTATTTTCKTGTGGCTAACTAGAACCAGAGTACAATGTTTCCAGTTCTT
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/note="Vect.or: pCMV-SPORT6"
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/tissue_type="cerebrum"
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OY 1799 ACCCTACATATCCTGAAGCTGAAAATAGAGATGGAGTGTAAGAGATTAACAACAGAATT 185  DD 1904 ATCCCACATATCCTGAAGATGAAATAGAGATGAAGTAGAGAGATTAACAACAAGAACT 196	Oy 1859 TAGTTCAGACCATCTCAGCCAAGCAGAAGACCCAGACTAACATATGGTTCATTGACAGAC 1910  Db 1964 CACTTCAGACCATCTCGGCCAAGCAGAAGACGCAGACTAACACGTGGTTCATTGATAGAC 2021	Qy         1919 ATGCTCCGCACCAAGAGCAAGTGGGAACCCTCAGATGCTGCACGTGGAACGCCTCTTT 1971           Db         2024 ACGCTCCACACCACCAAGAGCAAGCGGAACCCTCAGATGCTGCACTGGAACGCCTCTTT 2081	Qy         1979         GTGAAGGCTGCTGTGCCCTCAAGCCCAT         2007           Db         2084         ATGAAGGCTGTGGTGCCCTCAAGCCCAT         2112	4 7 BD168517 ION Cells produc ON BD168517	eosto	e s	L1B WA		FI YUTAKA KANDA,MILSUU SAIO,KAZATASU NAKANUKA,KAZOHLSA UCHIDA, PI POYOHIDE SHINKAWA,NAOKO YAMANB,EMI HOSAKA,MOTOO YAMASAKI,NOBUO PI HANDI PC C12N5/10,C12P21/08,C07K16/00,A01K67/00,A61K39/395,C12N9/00, PC	C12N15/52, PC G01N33/53 CC Cells producing antibody composition FH Key Location/Qualifiers	sour	/ Organism="Mus musculus" / mol_type="genomic DNA" / db_xref="texton:10090" DASE COUNT 529 a 365 c 400 g 434 t	Query Match Query Match Best Local Similarity 94.8%; Pred. No. 0; Matches 1638; Conservative 0; Mismatches 90; Indels 0; Gaps 0	GCGGGCATGGACTGGTTCCTGGCGTTGGATTATGCTCATTCTTTTTGCCTCGG	160 TTATTGTTTTATATAGGTGGTCATTTGGTTCGAATAATGACCACCCTGACCATTCTGGC 21	Qy 220 AGAGAACTCTCCAAGATTCTTGCAAAGCTGGAGCGTTAAAACAACAAAAAAAA

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/ voidence=experimental
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AIYAHQPFTADEI PWEPGDIIGVAGNHWDGYSKGVNRKLGRTGLYPSYKVREKIETVK
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Pred. No. 0;
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                   /codon start=1
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Best Local Similarity 87.5
Matches 1781; Conservative
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/EC_number="2.4.1.68"
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GGCCAAAATGCCCACAACCAGATTGCAGTTTATCCTCACCAACCTCGAACTAAAGAGGAA 1659
                                                                                                                                                                                                                                                                                                                                                                                          AAAGGTGTCAACAGAAAACTAGGAAAAACAGGCCTGTACCCTTCCTACAAAGTCCGAGAG 1779
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Homo sapiens mRNA for alpha6-fucosyltransferase (FUT8 gene), clone
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                    GACTITITIAGIGIACTITITICATCCCAGGICTGICICITITICATGAAATCATGCAA
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                                                                                                                     GACTTCCTTGTGTGTGTACTTTTTCATCCCAGGTCTGTAGGGTTGCTTATGAAATCATGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGATAGAAACAGTCAAATACCCTACATATCCTGAAGCTGAAAATAG 1827
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AJ539535.1 GI:28200807
alpha6-fucosyltransferase; FUT8 gene.
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Submitted (31-JAN-2003) Oriol R., U5
Vaillant-Couturier, 94807, FRANCE
Location/Qualifiers
1. 2796
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Homo sapiens
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Unpublished
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KEYWORDS
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8 6 8 6 6

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                                                                                                                                                                                      ----ACTAACATATGGTTCATTGACAGACATGCTCCGCACCAAGAGCAAGTGGGAACCCT 1949
                                                                                                                                                                                                            PRI 17-SEP-1998
1965 TGGGAAGGACGGGCCTATATCCCTCCTACAAGTTCGAGAAGATAGAAACGGTCAAGT 2024
                                                                         2025 ACCCCACATATCCTGAGGCTGAGAATAAAGCTCAGATGGAAGAGATAAACGACCAAACT 2084
                                                                                                                                                 2085 CAGTTCGACCAAACTCAGTTCAAACCATTTGAGCCAAACTGTAGATGAAGAGGGCTCTGA 2144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                           HSY17976 2898 bp mRNA linear PRI 17-SEP-1
Homo sapiens mRNA for glycoprotein 6-alpha-L-fucosyltransferase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cailleau, A.L.V.
Direct Submission
Submitrac (19-AUG-1998) A.L.V. Cailleau, INSERM U178, 16 av P.V.
Couturier, 94807 Villejuif Cedex, FRANCE
Related entry: D89289.
Location/Qualifiers
                                                                                                                                                                                                                                                                                      CAGATGCTGC-ACTGGTGGAACGCCTCTTTGTGAAGGGCTGCTGTGCCCTCAAGCC 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cailleau, A., Balanzino, L., Candelier, J.J., Oriol, R. and Mollicone, R.
Differential splice variants of human FUT8 embryonic CDNA Unpublished
                                                                                                              ----CAACAGAATITAGTICAGACCATCTCAGCCAAGCAGAAGACCCAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y17976.1 GI:3451262
FUTB gene; glycoprotein 6-alpha-L-fucosyltransferase.
Homo sapiens (human)
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GYGCOLHHVVYCFMIAYGPTILLESQNWRYATGGWETVFRPUSETCTDRSGISTGH
WASGEWROKVNQVVELEPTOSLHRRPRYTDLANPREDDLADRLKYNGDDFNWWWSQFYKT
LIROQWMLEKEIEEATKKLGFYGHYIGVHVRRTDKVGTFBAFPIEETWWYHGFFFFY
LIARRQVDKKRVYLATDDPSLIKEAKTKYPNYETSDNSISWSAGLHNRYTENSLRGV
ALIDIHELSQADFLVCTFSSQVCRVAYEEMQTLHPDASANFHSLDDIYYFGGQNAHNQI
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KILAKLBRLKQQNEDLARMAESLRIPEGPIDQGPAIGRVRVLEEQLVYKAKEQIENYKK
KTRNGLGKDHEILRRRIEUGAKELWFPLQSELKKLKNLEGNELQRHADBFLLDLGHHB
RSIMTDLYYLGQTGGADDWREKEAKDLFELVQRRITYLQNPKDCSKAKKLVCNINKGC
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Homo sapiens mRNA for alpha6-fucosyltransferase (FUT8 gene), clone
DCD-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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               TGGGAAGGACGGGCCTATATCCCTCCTACAAGTTCGAGAAGATAGAAAAATAAGAAAGT
                                                                       ACCCACATATCCTGAGGCTGAGAAATAAAGCTCAGATGGAAGAGATAAACGACCAAACT
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                                                        ACCCTACATATCCTGAAGCTGAAAATAGAGATGGAGTGTAAGAGATTAA
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/protein_id="CAD62445.1"
/db_xref="GI:28200810"
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/dev_stage="40-70 days"
/country="France:Paris"
1. .2902
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Submitted (31-JAN-2003) Oriol R.,
Vaillant-Couturier, 94807, FRANCE
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens
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alpha6-fucosyltransferase; FUT8
Homo sapiens (human)
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/gene="FUT8"
/EC_number="2,4.1.68"
/function="adds fucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="14"
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Splice variants of
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LIRPOPWLEKSI EBEYKKLGFKHPYLGVHYRRTDKVGTPBAFHPIEBYWVHYBEHFQL
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AIYAHQPRTAÑEIPMEPGDIIGVAGNHWDGYSKGVNRKLGRTGLYPSYKVREKIETVK
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               /codon start=1
/product="91/coprotein 6-alpha-L-fucosyltransferase"
/proten id="CAA76986.1"
/db_xref="G1:3451265"...
                                                        CAGATGCTGC-ACTGGTGGAACGCCTCTTTGTGAAGGGCTGCTGTGCCCTCAAGCC
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Catarrhini; Hominidae; Homo
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Submitted (19-AUG-1998) A.L.V. Cailleau, INSERM U178, 16
Couturier, 94807 Villejuif Cedex, FRANCE
Related entry: D89289.
Location/Qualifiers
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                                                                                                                                                                                                                                  FUTB gene; glycopiotein 6-alpha-L-fucosyltransferase.
Homo sapiens (human)
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2758. .2763
/gene="FUT8"
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QIRNGLGKHBILRRIENGREMEVERPELOSELKKLKNLEGDNELQRHADEFLLDIGHHE 
QIRNGLGKYLSQTDGAGDMEKEAKOLTELVQRRITYLQNPKDCSKAKKLVCNINKGC 
GYGCQLHHVYYCPMAYGYQRTLILESQNWRYATGGMETVFRPVSETCTDRSGISTGH 
WSGEVKDKNVQVVELPIVDSLHPRPPYLPLAVPEDLADRLVRVHGDPAVWWVSQFVKY
                                                                                       ----ACTAACATATGGTTCATTGACAGACATGCTCCGCACCAAGAGCAAGTGGGAACCCT 1949
CAGTICGACCAAACTCAGTICAAACCATITGAGCCAAACTGTAGAIGAAGAGGGCTCTGA 2247
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LARRMQVDKKRVYLATDDPSLLKEAKTKYPNYEPISDNSISWSAGLHNRYTENSLRGV
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (19-AUG-1998) A.L.V. Cailleau, INSERM U178, 16 av P.V.
Couturier, 94807 Villejuif Cedex, FRANCE
                                                                                                                                                                                                                                  HSY17978 11near PRI 06-NOV-:
Homo sapiens mRNA for glycoprotein 6-alpha-L-fucosyltransferase
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fyrotein id="chA76887.1"
db_xref="g1:3451267"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATACTACCTCAGTCAAACAGATGGAGCAGGTGAGTGGCGGGAAAAAAGAAGCCAAAGATC
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                                                                                                                                                                                                                                                                                                                                                                             AACAGAAACTTATTTCCTGTGTGGCTAACTAGAACCAGAGTACAATGTTTCCAATTCTT
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                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                             9; Length 3568;
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                                                                                                                                                                                                                                                                                                                              223;
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                                                                                                                                                                                                                                                                             Score 1575.2;
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/gene="FUT8"
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751 c
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87.5%;
                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Simil
Matches 1781; C
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                                                                             2475
                                                                                                                              1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO SADIENS MRNA For alpha6-fucosyltransferase (FUT8 gene), splice variant B5.
                                                                                                                                                                                                                                 1949
                                                                                                                                                                                                                                                             KITAKLERLKQQNEDLRRMAESLRIPEGPIDQGPAIGRVRVLEEQLVKAKEQIENYKK
QTRNGLGKDHEILRRIENGAKELWFFLQSELKKLKNLEGNELQRHADEFLLDLGHHE
RSIMTDLYYLSQTDGAGDWREKEAKDLTELVORRITYLQNPROCSKAKKLVCNINKGC
RSQCQLHHVVYCFMIAYQTORTLILESQNWRYATGGWFTVPRPVSETCTDRSGISTGH
WSGEVKUNKQVVCEPPIVDSLHPRPPYLDLAVPEDLADRLVRYHGDPAWWYSGPVKY
LIRPQPWLEKEIEBATKKLGFKHPVIGVHVRRTDKVGTEAAFHPIESYMVHVEBHFQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ĕ
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Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                 CAGATGCTGC-ACTGGTGGAACGCCTCTTTGTGAAGGGCTGCTGTGCCCTCAAGCC 2004
                                                                                                                                                                                                                                                                                                                                                                               2651
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/function="adds fuc in alphal,6 to the internal GlCNAc
                                                                                                                                                                                                                                 ----ACTAACATATGGTTCATTGACAGACATGCTCCGCACCAAGAGCAAGTGGGAACCCT
                                                                             2416 ACCCCACATATCCTGAGGCTGAGAATAAAGCTCAGATGGAAGAGATAAACGACCAAACT
                                                                                                                                                                                CAGTICGACCAAACTCAGTICAAACCATTTGAGCCAAACTGTAGATGAAGAGGGCTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mollicone, R., Michalski, J.C., Bauvy, C., Cailleau-Thomas, A., Candelier, J.J., Martinez-Duncker, I., Breton, C., Codogno, P. and Oriol, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (06-JAN-2003) Oriol R., U504, INSERM, 16 Avenue Paul
Vaillant-Couturier, Villejuif, 94807, FRANCE
related splice variants AU536053.1, AU536054.1 and AU536056.1.
                                                                                                                                                                                                                                                                                                                                                             CATAGGCTTCAATTGGTGGAATTCCTCTTTAACAAGGGCTGCAATGCCTCATACCC
                                                                                                                              ----CAACAGAATTTAGTTCAGACCATCTCAGCCAAGCAGAAGACCCAG
                                 ACCCTACATATCCTGAAGCTGAAAATAGAGATGGAGTGTAAGAGATTAA
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'protein_id="CAD59926.1"
'db_xref="GI:27552400"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="whole embryo"
/dev_stage="40-70 days"
/coultry="France:Paris"
| . .3568
/gene="FUT8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha6-fucosyltransferase; FUT8
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; (Primates; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the core chitobiose"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AJ536055
AJ536055.1 GI:27552399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .098. .2825
'gene="FUT8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 3568)
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
HSA536055
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AUTHORS
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JOURNAL
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/product="alpha6-fucosyltransferase"
|protein_id="CAD593924"|
| protein_id="CAD593924"|
| db_xref="d1:2752386"|
| trānslation="MRPWTGSWRWIMLILFAWGTLLFYIGGHLVRDNDHPDHSSRELS
| trānslation="MRPWTGSWRWIMLILFAWGTLLFYIGGHLVRDNDHPDHSSRELS
| triaAthark.QQNBDharwabslarlerger] togranglation-thangerlation-thanger
| QTBNGLGKOHBILLRRIENGRAFELWFFLQSELKKLNDLEGNBLQRHADFFLLDLGHH
| RSIMTDLYYLSQTDGAGDWREKEAKDLTELVQRRITYLQNPKDCSKAKKLVCNINKGC
                                                                                                                                                                                                                                                                                                                                                                                                                          Splice variants of alpha6-fucosyltransferase are expressed early in human embryogenes:s
Unpublished
                                                                                                                                       HOMO Sapiens MRNA for alpha6-fucosyltransferase (FUT8 gene), splice variant B3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GYGCQLHHVVYCFMIAYGTQRTLILESQNWRYATGGWETVFRPVSETCTDRSGISTGH
WSGEVKDKNYQVVELPIVDSLHPRPPYLPLAVPEDLADRLVRVHGDPAVWWVSQFVKY
LIRPQPWLEKSIEEATKKLGFKHPVIGVHVRRTDKVGTEAAFHPIEEYWVHVEEHFQL
LARRWQVDKKRYYLATDDPSILKEAKTKYPNYEFISDNSISWSAGLHNRYTENSLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILDIHFLSQADFLVCTFSSQVCRVAYEIMQTLHPDASANFHSLDDIYYFGGQNAHNOI
AIYAHQPRTADEIPWEPGDIIGVAGNHWDGYSKGVNRKLGRTGLYPSYKVREKIETVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EC number="2.4.1.68"
function="adds fuc in alpha1,6 to the internal GlcNAc of
                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                   Direct Submission
Submitted (06-JAN-2003) Oriol R., U504, INSERM, 16 Avenue
Vaillant-Couturier, Villejuif, 94807, FRANCE
related splice variants Ab336054.1, AJ536055.1 and AJ536056.1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  Mollicone, R., Michalski, J.C., Bauvy, C., Cailleau-Thomas, A., Candelier, J.J., Mirtinez-Duncker, I., Breton, C., Codogno, P.
              CAGATGCTGC-ACT(GTGGAACGCCTCTTTGTGAAGGGCTGCTGTGCCCTCAAGCC
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                               gene.
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trissue_type="whole embryo"

/dev.stage="40-70 days"

/country="France:Paris"

1. .3666
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                                                                                                                                                                                                                                                             FUT8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'evidence experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the core chitobiose"/codon_start=1
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                                                                                                                                                                                                                                      AJ536053.1 GI:27552395
alpha6-fucosyltransferase;
Homo sapiens (human)
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/AIYAHOPRTAREN
// AIYAHOPRTAREN
                                                                                                                                                                         Oriol, R. Splice variants of alpha6-fucosyltransferase are expressed early in Unpublished
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                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /EC number="2.4.1.68"
/function="adds fuc in alpha1,6 to the internal GlcNAc
the core chitobiose"
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                                                                                                                                                                                                                                                                                                                                                     Submitted (06-JAN-2003) Oriol R., U504, INSERM, 16 Avenue Paul Vaillant-Couturier, Villejuif, 94807, FRANCE related splice variants AJ536053.1, AJ536055.1 and AJ536056.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                       Mollicone, R., Michalski, J.C., Bauvy, C., Cailleau-Thomas, A., Candelier, J.J., Martinez-Duncker, I., Breton, C., Codogno, P.
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Pred. No. 0;
0; Mismatches 223;
                         FUT8 gene
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1. .3772
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organism="Homo sapiens"
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                         alpha6-fucosyltransferase;
Homo sapiens (human)
Homo sapiens
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larity 87.5%;
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gene="FUT8"
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3757
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Direct Submission
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                                          Oriol,R.
Direct Submission
Submitted (06-JRN-2003) Oriol R., U504, INSERM, 16 Avenue Paul
Submitted (06-JRN-2003) Villejuif, 94807, FRANCE
vaillant-Couturier, Villejuif, 94807, FRANCE
related splice variants AJ536053.1, AJ536054.1 and AJ536055.1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="whole embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1575.2;
Pred. No. 0;
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/chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                       dev_stage="40-70 days"
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/evidence=experimental
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llarity 87.5%;
Conservative
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4181
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1726. .3453
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                            (bases 1 to 4196)
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Oriol,R.
Splice variants of alpha6-fucosyltransferase are expressed early in human embryogenesis
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Homo sapiens MRNA for alpha6-fucosyltransferase (FUT8 gene), splice
variant B6.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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  CAGACAAAGTGGGAACAGAAGCTGCCTTCCATCCCATTGAAGAGTACATGGTGCATGTTG
                                                         CCACTGATGACCCTTCTTTGTTAAAGGAGGAGAAAGACAAAGTACTCCAATTATGAATTTA
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alpha6-fucosyltransferase; FUT8 gene.
Homo sapiens (human)
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E15725 2100 bp DNA linear PAT 28-JUL-1999 Human mRNA for alpha-1,6-fucosyltransferase, complete cds. E15725 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases I to 2100)

Taniguchi, N., Uozumi, H. and Yanagiya, S.
ALPHA-1, 6-PUCOSYLTFANSFERAS GENE DERLVED FROM HUMAN
Patent: JP 1998084575-A 1 07-APR-1998; TOYONCO CLID
OS Homo sapiens (human)
NO 17-APR-1998
PF 17-JUN-1997 JP 1997159692
PR 22-JUL-1996 JP 996 192260
PI TANIGUCHI NAOYUKI, UOZUMI HISAFUMI, YANAGIYA SHUSAKU PC
C12N15/09, C07H21/04, C12N1/21, C12N9/10, (C12N15/09, C12R1:91), PC

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### ALIGNMENTS

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Antibody production, cytostatic, immunomodulator, vasotropic, virucide, antibacterial; antiinflammatory; antiallergic, allergy, inflammation; autoimmune disease, Chinese hamster ovarian tissue-originated cell; CHO; tumour; dirculatory disease, infection; primer; ss.
                                                                                                                                                                                                                                                                                                                                        Shinkawa T, Yamane N;
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Yamano K, Yamasaki M, Hanai N;
                                                                                                Antibody production method related cDNA #1
                        ABK70031 standard; cDNA; 2008 BP.
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WPI; 2002-340182/37

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Cells producing antibody compositions including antibody fragments and tusion proteins with Fc domain of antibody, useful for prevention or treatment of cancer, immune diseases, circulatory diseases and infections - Claim 13; Page 1-3; 314pp; Japanese.

Claim 13; Page 1-3; 314pp; Japanese.

This invention relates to novel method for antibody production comprising a Chinese hamster ovarian tissue-originated (CHO) cell transferred with a gene encoding an antibody molecule for producing a composition comprising an antibody molecule with an Fc domain bonded to the V-glycoside linkage complex sugar chain. The produced antibody compositions are drugs for prevention or treatment of diseases, circulatory diseases, and viral and bacterial infections. The antibodies can be stably produced using the method of the invention with high binding activity and potency thus leading to high safety and aruges for therapy. The present sequence represents a nucleotide molecule used in the method of the invention.

Sequence 2008 BP; 626 A; 425 C; 465 G; 492 T; 0 other;

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100.0%; Score 2008;
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λ	CTGATGACCTTCTTTGTTAAAGGAGGCAAAGACAAAGTACTCCAATTATGAATTTATT 138
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අ <u>ප</u>	TCTATTTCTTGGTCAGCTGGACTACACAACCGATACACAGAAAATTCACTT 14
λ	441 CGGGGGCGTGATCCTGGATATACACTTTCTCTCCCAGGCTGACTTCCTTGTGTGTACTTTT 150
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δ	1561 GCAAACTTCCATTCTTTACATGACATCTACTATTTTGGAGGCCAAAATGCCCACAACCAG 1620
අු	caaacticcatictitagaigacaictactatitiggaggccaaaaigcccacaacag 162
ò	1621 ATTGCAGTITATCCTCACCACCACGAACTAAAGAGGAAATCCCCATGGAACCTGGAGAT 1680
අු	tigcagittaticticaccaaccicgaactaaagaggaaateeecatggaactiggagat 168
ò	681 ATCATTGGTGTGGGAAACCATTGGAATGGTTACTCTAAAGGTGTCAAAAAACTA 174
<b>a</b>	81 ATCATTGGTGTGGCTGGAAACCATTGGAATGGTTACTCTAAAGGTGTCAACAGAAACTA 1/4
ò	1741 GGAAAACAGGCCTGTACCCTTCCTACAAGTCCGAGAGAAGATAGAAACAGTCAAATAC 1800

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(a) assessing whether a patient is affiliated with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

(e) selecting a composition for inhibiting prostate cancer in a patient;

(f) assessing the prostate cell carcinogenic potential of a compound;

(f) assessing the aggressiveness or indolence of prostate cancer in a patient;

(h) assessing the aggressiveness or indolence of prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                             GGAAAAACAGGCCTGTACCTTCCTACAAAGTCCGAGAGAAAGATAGAAACAGTCAAATAC
                      CCTACATATCCTGAAGCTGAAAATAGAGATGGAGTGTAAGAGATTAACAACAGAATTTA
                                 CCTACATATCCTGAAAAATAGAGATGGAGTGTTAAGAGATTAACAACAGAATTTA
                                                             GCTCCGCACCAAGAGCAAGTGGGAACCCTGAGATGCTGCACTGGTGGAACGCCTCTTTGT
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
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                                                                                                                            cytostatic; carcinogen; pharmacodyanamic marker; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
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                 standard; cDNA; 3291
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2000US-189862P.
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16-MAR-2000;
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13-DEC-2000;
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179 GTGATTTGGTTCGAGATATGACACCCTGACCATTTCTAGGAGAGACTCTCCGAGATTC   238     180 GTGATTTGGTTCGAGGGTTATGACATCCTGACTCTCTGAGGAGATCTCCCAGATTC   258     181	959 AAGTGGTCCCCCATTGTAGACAGCCTCCTCCTTACTTACCCTTGG 1018  1586 AAGTGGTCCAGACTCCCATTGTAGACAGCCTCCTCCTTACTTA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to novel method for antibody production comprising a Chinese hamster ovarian tissue-originated (CHO) cell transferred with a gene encoding an antibody molecule for producing a composition comprising an antibody molecule with an Fc domain bonded to the N-glycoside linkage complex sugar chain. The produced antibody compositions are drugs for prevention or treatment of diseases accompositions are drugs for prevention or treatment of diseases, circulatory diseases, and viral and bacterial infections. The antibodies can be stably produced using the method of the invention with high binding activity and potency thus leading to high safety and reduced side effects when applied alone or in combination with other molecule used in the method of the invention.
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                                                                                                                             Cells producing antibody compositions including antibody fragments ar fusion proteins with Fc domain of antibody, useful for prevention or treatment of cancer, immune diseases, circulatory diseases and
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                                                                      Shinkawa T,
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                                                                    Uchida K,
, Hanai N;
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                                                                      Nakamura K, Ud
, Yamasaki M,
                                              (KYOW ) KYOWA HAKKO KOGYO KK
05-OCT-2001; 2001WO-JP08804
                       06-OCT-2000; 2000JP-0308526
                                                                    Satoh M, N
Yamano K,
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                          1680
AAAGGTGTCAACAGAAAACTAGGAAAAACAGGCCTGTACCTTCCTACAAAGTCCGAGAG 1779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
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                                                                                                                                                                                                                                                                 Human; colon cancer; colon cancer antigen; diagnosis; detection;
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                                                       AAGATAGAAACAGTCAAATACCCTACATATCCTGAAGCTGAAAATAG 1827
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N.B. Pages 666 to 6
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AAT76574 standard;

(first entry)

05-MAR-1998

AAT76574;

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human alpha 1-6 fucosyltransferases of the invention, respectively. The encoded enzyme transferases of the invention, respectively. The encoded enzyme transfers fucose from guanosine diphosphate to the encoded enzyme transfers fucose from guanosine diphosphate to the encoded enzyme respect molecule:

C. GlcNacbeta 1-2Manalpha 1-6) (GlcNacbeta 1-2Manalpha 1-3) Manbeta
C. 1-4GlcNAcbeta 1-4GlcNAc-R to give (GlcNacbeta 1-2Manalpha 1-6) (GlcNacbeta 1-4GlcNacheta 1-4GlcNacheta 1-4GlcNacheta 1-4GlcNacheta 1-6GlcNac-R. It has an optimum pH of about 7.0 (pig) or 7.5 (human), and is stable over the can optimum pH of about 7.0 (pig) or 7.5 (human), and is stable over the can enzyme is 30-37 degrees C. The optimum working
C. temperature of the enzyme is 30-37 degrees C. A bivalent metal is not required for activity of the enzyme, and the enzyme is not inhibited in the protection of sugar chains, and as antigen for the production of antibodies recognising the enzyme. The antibodies can be used for the carper and other diseases.
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                                           Alpha 1-6 fucosyltransferase; enzyme; pig; human; fucose transfer; guanosine diphosphate; sugar chain synthesis; modification; antibody; GlcNAc; cancer diagnosis; ss.
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synthesis and modification of sugar chains and used as an antigen
for production of diagnostic antibodies
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             Human alpha'1-6 fucosyltransferase gene.
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                                                                                        transferase; alphal,6-FT;
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          CCACTGATGACCCT'ICTTTGTTAAAGGAGGCAAAGACAAAGTA
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GTCACTTGGTACGAGATAATGACCATCCTGATCACTCTAGCCGAGAACTGTCCAAGATTC
                   AAGAACAGCTTGTTAAGGCCAAAGAACAGATTGAAAATTACAAGAAACAAGCTAGGAATG
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                                                                                                                                                                                                                               The invention relates to a plant cell with an animal type sugar chain adding function, created by transforming a tobacco cell with a gene encoding an enzyme derived from an animal which can transfer a fucose residue to the reductive end acetylglucosamine residue of a sugar chain. The gene that is introduced into the plant cell encodes the enzyme alphal, 6-fucosyl transferase. The method of the invention is useful for the preparation of a glycoptcein having animal type sugar chain. The current sequence represents alphal, 6-fucosyl transferase cDNA.
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                                                                                                   A plant cell with an animal type sugar chain adding function, preparation of a glycoprotein with an animal type sugar chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 75.4%; Score 1514.8; DB 24; Lengt
Best Local Similarity 92.1%; Pred. No. 0;
Matches 1597; Conservative 0; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1759 BP; 533 A; 367 C; 418 G; 441 T; 0 other;
                                                                                                                                                                                   Example 1; Page 22-24; 38pp; Japanese
                           2002-158816/21
                           WPI; 2002-158816/
P-PSDB; ABB08405
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                                                                                                               Alpha 1-6 fucosyltransferase; enzyme; pig; human; fucose transfer; guanosine diphosphate; sugar chain synthesis; modification; antibody; GlcNAc; cancer diagnosis; ss.
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                                                                          Pig alpha 1-6 fucosyltransferase gene
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                                                                                                                                                                                                                                                                                                                                                                                        Immunologically functional molecule; immune system; immunomodulation; glycosylation; fucose; N-acetylglucosamine; cancer; circulatory disease; viral infection; bacterial infection; allergy; autoimmune disease; inflammation; antibody; Chinese hamster; FUT8; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Control of activity of antibodies and other immunologically functional molecules by addition or removal of fucose from sugar chain for diagnosis and treatment of cancer, allergy and other diseases -
CGATATACAGAAAATTCACTTCGGGGTGTGATACTCTGGATATACACTTTCTCTCCCCAGGCA
                                                                        CGATACACAGAAAATTCACTTCGGGGCGTGATCCTGGATATACACTTTCTCTCCCAGGCT
                                                                 GACTTCCTTGTGTGTATATTTTTCATCCCAGGTCTGTAGGGTTGCTTATGAAATCATGCAA
                                                                                                    1540 ACACTGCATCCTGATGCCTCTGCAAACTTCCATTCTTTAGATGACATCTACTATTTTGGA
                                                                                                              GCGCTGCATCCTGATGCCTCTGCGAACTTCCGTTCTTTGGATGACATCTACTATTTTGGA
                                                                                                                                         GGCCAAAATGCCCACACCAGATTGCAGTTTATCCTCACCAACCTCGAACTAAAGAGGAA
                                                                                                                                                   GGCCCAAAIGCCCACAAATTGCCATTTATCCTCACCAACCTGAACTGAAGGAGAA
                                                                                                                                                                            1660 ATCCCCATGGAACCTGGAGATATCATTGGTGTGGCTGGAAACCATTGGAATGGTTACTCT
                                                                                                                                                                                       AAAGGTGTCAACAGAAAACTAGGAAAAACAGGCCTGTACCTTCCTACAAAGTCCGAGAG
                                                                                                                                                                                                                                  AAAGGTGTTAACAGAAACTGGGAAGGACGGCCTATATCCCTCCTACAAAGTTCGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for controlling the activity of an immunologically functional molecule (e.g., an antibody) where the control is effected by the presence or absence of fucose bound to an
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Anazawa P
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Yamane 1
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S, Kanda Y,
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N-acetylglucosamine residue at the reducing end of the sugar chain on the immunologically functional molecule. The invention also relates to methods for the diagnosis, prevention or treatment of diseases which involve the modified immunologically functional molecule, and agents which stimulate the activity of an immunologically functional molecule. The methods of the invention are used for the diagnosis, treatment and prevention of a broad range of diseases including cancer, circulatory disease, viral or bacterial infection, allergy, autoimmune disease and inflammation. The present sequence represents a Chinese hamster FUT8 cDNA isolated in an exemplification of the invention.
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Pred. No. 7.6e-280;
0; Mismatches 1;
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   AATCCCCATGGAACCTGGAGATATCATTGGTGTGGCTGGAAACCATTGGAATGGTTACTC 1718
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                                                                                                                                                                                                                                                         Antibody production; cytostatic; immunomodulator; vasotropic; virucide; antibacterial; antiinfammatory; antiallergic; allergy; infilammation; autoimmune disease; Chinese hamster ovarian tissue-originated cell; CHO; tumour; circulatory disease; infection; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to novel method for antibody production comprising a Chinese hamster ovarian tissue-originated (CHO) cell transferred with a gene encoding an antibody molecule for producing a composition comprising an antibody molecule with an Fc domain bonded to the N-glycoside linkage complex sugar chain. The produced antibody compositions are drugs for prevention or treatment of diseases accompositions are drugs for prevention or treatment of diseases, circulatory diseases, and viral and bacterial infections. The antibodies can be stably produced using the method of the invention with high binding activity and potency thus leading to high safety and reduced side effects when applied alone or in combination with other molecule used in the method of the invention.
                                                          TAAAGGTGTCAACAGAAAACTAGGAAAAACAGGCCTGTACCTTCCTACAAAGTCCGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cells producing antibody compositions including antibody fragments an fusion proteins with Fc domain of antibody, useful for prevention or treatment of cancer, immune diseases, circulatory diseases and
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99.9%; Pred. No. 7.6e-280;
cive 0; Mismatches 1;
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Hanai N;
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Yamasaki M,
                                                                                          GAAGATAGAAACAGTCAA 1796
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Yamano K,
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Antibody production; cytostatic; immunomodulator; vasotropic; virucide; antibacterial; antiinflammatory; antiallergic; allergy; inflammation; autoimmune disease; Chinese hamster ovarian tissue-originated cell; CHO; tumour; circulatory disease; infection; primer; ss.
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                                                                                               Immunologically functional molecule; immune system; immunomodulation; glycosylation; fucose; N-acevylglucosamine; cancer; dirculatory disease; viral infection; bacterial infection; allergy; autoimmune disease; inflammation; antibody; rat; FUT8; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method for controlling the activity of an immunologically functional molecule (e.g., an antibody) where the control is effected by the presence or absence of fucese bound to an N-acetylglucosamine residue at the reducing end of the sugar chain on the immunologically functional molecule. The invention also relates to methods for the diagnosis, prevention or treatment of diseases which involve the modified immunologically functional molecule. The methods of the activity of an immunologically functional molecule. The methods of the invention are used for the diagnosis, treatment and prevention of a broad range of diseases including cancer, circulatory disease, viral or bacterial infection, allergy, autoimmune disease and inflammation. The present sequence represents a rat FUT8 cDNA isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Control of activity of antibodies and other immunologically functional molecules by addition or removal of fucose from sugar chain for diagnosis and treatment of cancer, allergy and other diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ACTCATCTTGGAATCTCAGAATTGGCGCTATGCTACTGGTGGTGGAGACTGTGTTTAG
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Pred. No. 4.5e-255;
...arrheg 53; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamasaki M,
Anazawa H;
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Yamane N,
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Best Local Similarity 94.6%;
Matches 925; Conservative (
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Imabeppu S, Kanda Y,
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                                                         Rat FUT8 cDNA
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                                    1419 CCGATACACAGAAAATTCACTTCGGGGGGGGGGGTGATCCTGGATATACACTTTCTCTCCCAGGC
                                                                                                                  1479 IGACTICCTIGIGIGIACITITICAICCCAGGICTGIAGGGITGCTIAIGAAATCAIGCA
                                                                                                                                                                                                                                 721 AACCCTGCATCCTGATGCCTCTGCAAACTTCCACTCTTTAGATGACATCTACTATTTTGG
                                                                                                                                                                                                                                                                          1599 AGGCCAAAATGCCCACAACCAGATTGCAGTTTATCCTCACCAACCTCGAACTAAAGAGGA
                                                                                                                                                                                                                                                                                                                                                                          Human, alpha 1-6 fucosyltransferase; alpha 1-6 fucT; antibody; alpha 1-6 fuccse transferase; anti-human alpha 1-6 fucCT; immunoassay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human alpha 1-6 fucosyltransferase 237-575 encoding DNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes an anti-human alpha 1-6 fucose fucosyltransferase (alpha 1-6 fucT, also called alpha 1-6 fucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/partial
/product= "alpha 1-6 fucosyltransferase 237-575"
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P-PSDB; AAB75061.
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                                                                                                                                                                                                                                                                                          This invention relates to novel method for antibody production comprising a Chinese hamster ovarian tissue-originated (CHO) cell transferred with a gene encoding an antibody molecule for producing a composition comprising an antibody molecule with an Fc domain bonded to the N-glycoside linkage complex sugar chain. The produced antibody compositions are drugs for prevention or treatment of diseases accompanying tumour, allergy or inflammation, autoimmune diseases, circulatory diseases, and viral and bacterial infections. The antibodies can be stably produced using the method of the invention with high binding activity and potency thus leading to high safety and reduced side effects when applied alone or in combination with other molecule used in the method of the invention.
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                                                                                                                                                         Cells producing antibody compositions including antibody fragments ar fusion proteins with Fc domain of antibody, useful for prevention or treatment of cancer, immune diseases, circulatory diseases and
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thes 53; Indels
                                                             Shinkawa T,
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                                                           Uchida K,
Hanai N;
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44.5%; Score 893.2;
Best Local Similarity 94.6%; Pred. No. 4.5e
Matches 925; Conservative 0; Mismatches
                                                                                                                                                                                                                                                           Example 9; Page 13-14; 314pp; Japanese
                                                                             Σ
                                                             ıkamura K,
Yamasaki №
                                                             Nakamura
                      (KYOW ) KYOWA HAKKO KOGYO KK
                                                         Satoh M, Na
Yamano K,
                                                                                                                      WPI; 2002-340182/37.
                                                         Kanda Y,
Hosaka E,
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transferase) antibody. Also described are: (1) a hybridoma producing the above monoclonal antibody; (2) an immunoassay for detecting human alpha 1-6 fucT by using the above antibody or its antibody fragment; and (3) a reagent used for the above immunoassay. The anti-human alpha 1-6 fucT antibody can be used for immunoassay. The present sequence encodes the human alpha 1-6 fucT protein of residues 237 to 575, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                  CTTCATCCCCGTCCTCCATATTTACCCTTGGCTGTACCAGAAGACCTCGCAGATCGACTT
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                                                                                                                         22; Length 1017;
                                                                                                              Score 881; DB 22; Lengtn 1. Pred. No. 2e-251;
                                                                                                 Sequence 1017 BP; 296 A; 231 C; 228 G; 262 T; 0 other;
                                                                                                                                               0; Mismatches
                                                                                                                       Query Match
Best Local Similarity 91.6%;
Matches 932; Conservative
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1708 AATGGTTACTCTAAAGGTGTCAACAAGAAACTAGGAAAACAGGCCTGTACCCTTCCTAC 1767
                                         901 GATGGCTATTCTAAAGGTGTCAACAGGAAATTGGGAAGGAGGACGCGCTATATCCCTCCTAC 960
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                                                                                                       AAAGTCCGAGAGAAGATAGAAACAGTCAAATACCCTACATATCCTGAAGCTGAAAAA 1824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes an anti-human alpha 1-6 fucose fucosyltransferase (alpha 1-6 fucT, also called alpha 1-6 fucose transferase) antibody. Also described are: (1) a hybridoma producing the above monoclonal antibody; (2) an immunoassay for detecting human alpha 1-6 fucT by using the above antibody or its antibody fragment; and (3) a reagent used for the above immunoassay. The anti-human alpha 1-6 fucT antibody can be used for immunoassay. The present sequence encodes the human alpha 1-6 fucT protein of residues 343 to 575, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAAAAAAGAAATAGAAAGAAGCCACCACCAAGAAGCTTGGAAGTTCAAACATCCAGTTATTGGAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, alpha 1-6 fucosyltransferase; alpha 1-6 fucT; antibody;
alpha 1-6 fucose transferase; anti-human alpha 1-6 fucT; immunoassay;
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91.1%; Pred. No. 8.8e-168;
cive 0; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 7-8; 11pp; Japanese.
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                                                                                                                                                                                                                                                                                                 BP.
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ATGGTACACGTTGAAGAACATTTTCAGCTTCTCGAACGCAGAATGAAAGTGGATAAAAA
           AGAGTGTATCTGGCCACTGATGACCCTTCTTTGTTAAAGGAGGCAAAGACAAAGTACTCC
                                                 AATTATGAATTTATTAGTGATAACTCTATTTCTTGGTCAGCTGGACTACAACCGATAC
                                                                                      ACAGAAAATTCACTTCGGGGCGTGATCCTGGATATACACTTTCTCTCCCAGGCTGACTTC
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                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL10511), expressed DNA sequences (ABL16176-ABL10511), expressed DNA
isolated nucleic acid detection reagent for detecting 1000 or more es from Drosophila and for elucidating cell signalling and cell-cell
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Search completed: February 2, 2004, 12:33:47 Job time : 556.385 secs

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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-232-463-14
US-09-134-001C-2083
US-09-173-300-18
US-09-627-122-21
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Sequence 7, Appli
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Sequence 105, App
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Sequence 1, Appli
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US-08-044-547-2
US-09-134-001C-2383
US-09-122-400B-12
US-09-134-001C-1821
US-09-134-001C-1821
US-09-512-342-2
US-09-512-342-2
US-09-134-001C-2485
US-08-134-001C-2485
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US-08-687-080-105
US-09-734-674-3
                                 US-09-643-990A-1
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GENERAL INFORMATION:

APPLICANT: TANIGUCHI, Nacyuki
APPLICANT: TANIGUCHI, Nacyuki
APPLICANT: SHIBA, Tetsuo
APPLICANT: SHIBA, Tetsuo
APPLICANT: YANAGIDANI, Shusaku
TITLE OF INVENTION: Albha 1-6 Fucosyltransferase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3+ Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WordPerfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,805A
FILING DATE: 7 JAN 1996
CLASSIFICATION: APPLICATION ATA:
APPLICATION WUMBER: PCT/JP97/00171
FILING DATE: 23 JAN 1997
APPLICATION NUMBER: UP 162813
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JAN 1996
ATHORNEY AGENT INFORMATION:
NAME: TOFFAMET: LANGTH INFORMATION:
; Sequence 9, Application US/03913805A ; Patent No. 6054304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Toffenetti, Judith L. REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2100 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 202-12.
TELEPHONE: 202-429-0796
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US-09-442-629-9
; Sequence 9, Application US/09442629
; Patent No. 6291219
; GENERAL INFORMATION:
; APPLICANT: TANIGUCHI, Nacyuki
; SHIEA, Tetsuo
; SHIEA, Tetsuo
; YANAGIDANI, Shusaku
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                                    Score 1568; DB 3;
Pred. No. 0;
0; Mismatches 185;
                                    Query Match
Best Local Similarity 90.0%;
Matches 1691; Conservative
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GCTTTTTCCTACAGAGTGAATTGAAGAATTTAAAGAACTTAGAAGGAAATGAACTCCAAA
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 TCCGGATACCAGAAGGCCCTATTGATCAGGGGCCAGCTATAGGAAGAGTACGCGTTTTAG
                                                            AAGAGCAGCTTGTTAAGGCCAAAGAACAGATTGAAAATTACAAGAAACAGACCAGAAATG
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 OF INVENTION: Alpha 1-6 Fucosyltransferase
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                                          ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W.,
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                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/913,805A
FILING DATE: 7 JAN 1998
APPLICATION NUMBER: PCT/JP97/00171
FILING DATE: 23 JAN 1997
APPLICATION NUMBER: JP 19260
FILING DATE: 22 JUL 1996
APPLICATION NUMBER: JP 162813
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JAN 1996
APPLICATION NUMBER: JP 10365
ATTORNEY AGGNT 1000:
                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WordPerfect 6.1 Windows
                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/442,629
FILING DATE: 18-NO. 6291219-1999
PRIOR APPLICATION DATA:
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 2356/3
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SEQUENCE DESCRIPTION: SEQ ID NO: 9:
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LENGTH: 2100 base pairs
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INFORMATION FOR SEQ ID NO: 9:
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STRANDEDNESS: double
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90.0%;
                NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS
                                                                                                                       ZIP: 20036
UTER READABLE FORM
                                                                           CITY: Washington STATE: DC
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Matches 1691; Conservative
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                1537 TTCGTGGAGTGATCCTGGATATACATTTTCTCTCTCAGGCAGACTTCCTAGTGTACTT
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STREBT: 1025 Connecticut Avenue, N.W., Suite
CITY: Washington
COUNTRY: US
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MEDIUM TYPE: 3 + Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOGTWARE: WordPerfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,805A
FILING DATE: 7 JAN 1998
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: PCT/JP97/00171
APPLICATION NUMBER: 1997
APPLICATION NUMBER: JP 192260
FILING DATE: 22 JUL 1996
APPLICATION NUMBER: JP 162813
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 162813
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 21 JUN 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: TANIGUCHI, Naoyuki
APPLICANT: TOUCUMI, Naofumi
APPLICANT: SHIBA, Tetsuo
APPLICANT: SANAGIDANI, Shusaku
TITHE OF INVENTION: Alpha 1-6 Fuc
CORRESPONDENCE ADDRESS:
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Patent No. 6054304
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FILING DATE: 24 JAN 1996
ATTORNEY/AGENT INFORMATION:
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US-08-913-805A-1
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                                                                                                                                                                                                                                                                                       Length 1728;
                                                                                                                                                                                                                                                                                   73.4%; Score 1474.2; DB 3; Length
90.9%; Pred. No. 0;
tive 0; Mismatches 158; Indels
             REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 2356/3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
TELEPHONE: 202-429-0796
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1728 base pairs
Toffenetti, Judith L.
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.9
Matches 1569; Conservative
                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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340 GGAAGAGTCCGTGTTTTAGAAGAACAGCTTGTTAAGGCCAAAGAACAGATTGAAATTAC 399
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Pred. No. 0;
0; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/913,805A
FILING DATE: 7 JAN 1998
APPLICATION NUMBER: PCT/1997/00171
FILING DATE: 23 JAN 1997
APPLICATION NUMBER: JP 19260
FILING DATE: 22 JUL 1996
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 10165
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JAN 1996
                                                                                                                                                                                           MEDIUM TYPE: 3+ Floppy disk
COMPUTER: 1BM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6
SOFTWARE: WordPerfect 6.1 Windows
                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/442,629
FILING DATE: 18-NO. 6291219-1999
PRIOR APPLICATION DATA:
                                                                 Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Toffenetti, Judith L.
REGISTRATION NUNBER: 39,048
REFERENCE/DOCKET NUMBER: 2356/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: cDNA
'SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Av
CITY: Washington
STATE: DC
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                ZIP: 20036
COMPUTER READABLE FORM:
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Best Local Simil
Matches 1569; C
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CCTGTAAGTGAGACGTGCACAGACAGATCTGGCAGCTCCACTGGACATTGGTCAGGTGAA 840
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                                                                                   GTAAAGGACAAAATGTTCAGGTGGTTGAGCTCCCCATTGTAGACAGTGTTCATCCTCGT
                                                                                                                                                                         CCTCCATATTTACCCCTGGCTGTCCCAGAAGACCTTGCAGATCGACTTGTACGAGTCCAT
                                                                                                                                                                                                                  GGTGATCCTGCAGTGTGGTGTATCCCAGTTTGTCAAATACTTGATCCGTCCACAACCT
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APPLICANT: TANIGUCHI, Naoyuki
UOZUMI, Naofumi
SHIBA, Tetsuo
YANAGIDANI, Shusaku
TITLE OF INVENTION: Alpha 1-6 Fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09442629
Patent No. 6291219
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Sequence 1, Application US/0900041A
Fatent No. 6191255
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL PROTEIN AND MONOCLONAL ANTIBODY SPECIFIC THERETO
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1297 ATAATTTCCCTGTGAAGATAGCAAGAGGTACACACACAACATAGCATCAAGCTGGATCAG 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1357 AAAGATTAATAATAATGATTAAATAGCTGTTGTTTCTTCTCATTCTGTTTCCCAAGAGGA 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1766 ACAAAGTCCGAGAAGAAGATAGAAACAGTCAAATACCCTACATATCCTGAAGCTGAAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1826 AGAGATGGAGTGAAGATTAACAACAGAATTTAGTTCAGACCATCTCAGCCAAGCAGA
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC
FILE REFERENCE: BB-1126
CURRENT APPLICATION NUMBER: US/09/173,300
CURRENT FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: 60/063,423
EARLIER FILING DATE: 1997 October 28
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Microsoft Word Version 7.0A
LENGTH: 1501
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                                                                                                                                                                                                                                                                                                                                                                                                Score 38.4; DB 4; Length 1501;
Pred. No. 0.37;
0; Mismatches 51; Indels 0.
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COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APLICATION NUMBER: US/09/000,041A
FILING DATE: January 13, 1998
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/01956
FILING DATE: July 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 40,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                1.9%;
Similarity 57.5%;
59; Conservative (
                                                                                                                                                                                                                                                                                                                    ORGANISM: Triticum aestivum US-09-173-300-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202-721-8250
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ORIGINAL SOURCE:
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
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                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                        326 AGGGGACAGCTACAGGAAGAGTCCGTGTTTTAGAAGAACAGCTTGTTAAGGCCAAAGAAC 385
                                                                                                             386 AGATTGAAAATTACAAGAAACAAGCTAGGAATGATCTCTGGGAAAGGATCATGAAATCTTAA 445
                                                                                                                                                                                                                  446 GGAGGAGGATTGAAAATGGAGCTAAAGAGCTCTGGTTTTTTCTACAAAGTGAATTGAAGA 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   626 CAGGTGAGTGGCGGGAAAAAGGAGCCAAAGATCTGACAGAGCTGGTCCAGCGGAGAATAA 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1070 RRRRATCGCAAGCTCCCTCGACCTGCAAGCTCGGAATTAATTCTGTGA 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           686 CATATCTGCAGAATCCCAAGGACTGCAGCAAAGCCAGAAAGCTGGTATGTAA 737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 CAAAGAACAGATTGAAAATTACAAGAAACAAGCTAGGAATGATCTGGG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 AAAAGAGAGAACCAAATTTTAAAAGAACAAGCTGAGAATGAACTGCG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2083, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-2083
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Patent No. 6451581
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APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
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1507 AATGAAAGAATGGACCCTGGCTATCCCAAGCCAATCACAGTCTGGAAAGGGATCCCTGA 1566
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                                                                                                                                                                                                                                         1627 GGAGTATTGGAAATTCAACAACCAGATACTCAAGGTAGAACCTGGACATCCAAGATCCAT 1686
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                                                                                                                       379 AAAGAACAGATTGAAAATTACAAGAAACAAGCTAGGAATGATCTCGGGAAAGGATCATGAA 438
                                                                                                                                                                                                      439 ATCTTAAGGAGGAGTTGAAAATGGAGCTAAAGAGCTCTGGTTTTTTCTACAAAG---- 494
                                                                                                                                                                                                                                                                                                                                                                 TCTTTTGGATTTAGGACATCATGAAAGGTCTATCATGACAGATCTATACTACCTCAGTCA 614
                                                                                                                                                                                                                                                                                   495 TGAATTGAAGAAATTAAAGAAATTAGAAGGAAACGAACTCCAAAGACATGCAGATGAAAT
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                                                                               Gaps
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APPLICANT: Gothe, Gislinde
APPLICANT: Gothe, Gislinde
APPLICANT: Schwerdel, Marc
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 02481.1678
FULE REFERENCE: 02481.1678
CURRENT APPLICATION UNBER: US/09/627,122
CURRENT FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 23
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                                     Score 37.6; DB 3; Length 2116;
Pred. No. 0.75;
0; Mismatches 124; Indels 4.
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Pred. No. 1.2;
0; Mismatches 64; Indels 0
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Patent No. 6472521
GENERAL INFORMATION:
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Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Bult et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-09-627-122-21
                                         1.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.9%;
Best Local Similarity 54.3%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                615 AACAGATGGAGCAG 628
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                                                          Best Local Similarity 49.6
Matches 126, Conservative
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Greiner, Beate
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US-08-916-421B-1/c
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LENGTH: 5340
US-09-000-041A-1
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                                         Query Match
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TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ Patent No. 6503729
TITLE REPERBUCE: PROPERTION: jannaschii
TITLE REPERBUCE: PROPERTION: jannaschii
CURRENT APPLICATION NUMBER: US/08/916,421B
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR PILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
SEQ ID NO.
LENGTH: 1664976
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OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (28222). (28222)
CTHER INFORMATION: nequals a, t,
NAME/KEY: misc_feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc_feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: nequals a, t,
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LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AME/KEY: misc feature
OCATION: (98343)..(98343)
YTHER INFORMATION: n equals a,
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ION: (231980)..(231980)
INFORMATION: n equals a,
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a,
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INFORMATION: n equals a,
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LOCATION: (103998)..(103998)
THER INFORMATION: n equals a,
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FION: (191989)...(191989)
R INFORMATION: n equals a,
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LOCATION: (234220)..(234220)
JTHER INFORMATION: n equals a,
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INFORMATION: n equals a,
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ION: (234187)..(234187)
! INFORMATION: n equals a,
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INFORMATION: n equals a,
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/OCATION: (148948)..(148948)
/THER INFORMATION: n equals a,
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INFORMATION: n equals a,
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INFORMATION: n equals
KEY: misc_feature
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INFORMATION: n equals
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FION: (98159)..(98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEY: misc_
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                                                                                                                                                                                                                                                         TYPE: DNA
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LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature NAME/KEY: misc\_feature LOCATION: (319226)...(319226) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (559167)...(559167) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (559241)..(559241) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature NAME/KEY: misc\_feature LOCATION: (657081) . (657081) OTHER INFORMATION: n equals a, AME/KEY: misc\_feature OCATION: (779455)..(779455) THER INFORMATION: n equals a, AME/KEY: misc feature COCATION: (779676)..(779676) THER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (855539)..(855539) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1310988)..(1310988) OTHER INFORMATION: n equals a, LOCATION: (657203)..(657203) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (674435)..(674435) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature\_ LCCATION: (713552)..(713652) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature AME/KEY: misc\_feature LOCATION: (871619)..(871619) THER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1119881)..(1119881) OTHER INFORMATION: n equals a, INFORMATION: n equals a, OCATION: (1096846)..(1096846) THER INFORMATION: n equals a, LOCATION: (309418) (309418) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (622708)..(622708) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (682442)..(682442) OTHER INFORMATION: n equals a, JOCATION: (741684)..(741684) LOCATION: (1084830)..(1084830) OTHER INFORMATION: n equals a, n equals a, LOCATION: (312837)..(312837) OTHER INFORMATION: n equals a, LOCATION: (600992)..(600992) OTHER INFORMATION: n equals a, NAME/KEY: misc feature GOCATION: (1313224)..(1313224) NAME/KEY: misc\_feature feature NAME/KEY: misc\_ THER

331793 TGTCTTAAGAGGCACCATTTGGATGTATAAGGCATTTAAAATCAGCTGTAAAGGACATCC 331734 331613 CATAAATATAAATAAAGATGAAGAGTTGTTAGCTTTAGCTAAACATGAATTGGGAATTA 331555 470 531 ACTCCAAAGACATGCAGATGAAATTCTTTTGGATTTAGGACATCATGAAAGGTCTATCA 589 411 TAGGAATGATCTGGGAAAGGATCATGAAATCTTAAGGAGGAGGATTGAAAATGGAGCTAA AGAGCTCTGGTTTTTTCTACAAAGTGAATTGAAGAAATTAAAGAAATTAGAAGGAAACGA TGTTTTAGAAGAACAGCTTGTTAAGGCCAAAGAACAGATTGAAAATTACAAGAAACAAGC 0; Gaps DB 4; Length 1664976; Query Match
1.9%; Score 37.4; DB 4; Length 16
Best Local Similarity 47.3%; Pred. No. 22;
Matches 113; Conservative 0; Mismatches 126; Indels NAME/KEY: misc feature LOCATION: (1664854)..(1664855); OTHER INFORMATION: n equals a, t, c, or g US-08-916-421B-1 φ ρ ρ p b b ö or or ö ö ö ϋ ΰ ΰ Sequence 2, Application US/09125287B Patent No. 6114602 GENERAL INFORMATION: NAME/KEY: misc feature
LOCATION: (1349491)...(1349491)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1470091)...(1470091)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (1602912)..(1602912) OTHER INFORMATION: n equals a, LOCATION: (1637998)..(1637998) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1569020)..(1569020) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1603734)..(1603734) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (1349473)..(1349473) OTHER INFORMATION: n equals a, equals NAME/KEY: misc\_feature US-09-125-287-2/c 351 ò В ò g 6 g ð g

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APPLICANT: BARG, Rivka
APPLICANT: BARG, Tenham
APPLICANT: SALTS, Tenham
TITLE OF INVENTION: METHOD FOR THE INTRODUCTION OF GENETIC PARTHENOCARPY IN
TITLE OF INVENTION: PLANTS
FILE REFERENCE: INTRO GENETIC PARTHENOCAPRI IN PLANTS
CURRENT APPLICATION NUMBER: US/09/125,287B
CURRENT PILLING DATE: 1998-11-09
EARLIER APPLICATION NUMBER: PCT/1L97/00051
BARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATCHILIN VET: 2.0

ORGANISM: TPRP-F1 PROMOTOR

SEQ ID NO 2 LENGTH: 4518

TYPE: DNA

us-09-971-773-1.rni

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336 ATTTGGAAGAACTCTTAAATCTCTAAATGATCTTGTTGATAAATATCAAAAACAAATCG 395
                                                                                                                                                                                                                               Sequence 139, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 AAGAAATTACAAAACAAATTGATTTTATCAAAAAAGTTGATGAAACTTTTAAACAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 CAGCTACAGGAAGAGTCCGTGTTTTAGAAGAACAGCTTGTTAAGGCCCAAAGAACAGATTG
                                                                    392 AAAATTACAAGAAACAAGCTAGGAATGATCTGGGAAAGGATCATGAAATCTTAAGG 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272 AAGACTTGAGGAGAATGGCTGAGTCTCTCCGAATACCAGAAGGCCCTATTGATCAGGGGA
                                                                                                                 396 AACTTTTGAAGAAGAAGAAGAAAAAAGCTGCTGAAAAAGCTGCTGAAAAGCAAAG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        392 AAAATTACAAGAAACAAGCTAGGAATGATCTGGGAAAGGATCATGAAATCTTAAGG 447
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WEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFCATION: CURROWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S: Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: 98340P3
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87;
                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 36.8; Di
50.6%; Pred. No. 0.8;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 139: US-09-536-784-139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 148, Application US/08961527; Patent No. 6420135; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 805 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 139
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20850
COMPUTER READABLE FORM:
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Best Local Similarity 50.6'
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELEFAX:
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US-08-961-527-148
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                                                                                                                         1586 TCTACTATTTTGGAGGCCAAAATGCCCACAACCAGATTGCAGTTTATCCTCACCAACCTC 1645
                                                                                                                                                                                                                1646 GAACTAAAGAGGAAATCCCCATGGAACCTGGAGATATCATTGGTGGGCTGGAAACCATT 1705
                                                                                                                                                                                                                                                                                                        1706 GGAATGGTTACTCTAAAGGTGTCAACAGAAAACTAGGAAAAACAGGCCTGTACCCTTCCT 1765
                                                                                                                                                       219 TCGCCTATTTGGGATGCATTATHHDSVANAASNATANNAYGSNTYADASNASNASCHVHNYHN 160
                                                                                                                                                                                                                                             276 AAGAAATTACAAAACAAATTGATTTTATCAAAAAAGTTGATGAAACTTTTAAACAAGAGA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 CAGCTACAGGAAGAGTCCGTGTTTTAGAAGACAGCTTGTTAAGGCCAAAGAACAGATTG 391
                                                                                                                                                                                                                                                                                                                                     272 AAGACTTGAGGAGAATGGCTGAGTCTCTCCGAATACCAGAAGGCCCTATTGATCAGGGGA
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae Antigens and Vaccines: 452
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                              Length 4518;
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                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                             GNASDANCYYAKYDAVCNHAGNNGGKNCYADAGNASVTA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
COFTWARE: ASCII Text
                            1.9%; Score 37.2; DB 3; I 22.8%; Pred. No. 1.4; tive 67; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87;
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Pred. No. 0.8;
0; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 139, Application US/08961083; Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.,
TITLE OF INVENTION: Streptococcus pr
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.6%;
Matches 89; Conservative
                                                                           50; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                              Query Match
Best Local Similarity
Matches 50; Conserv?
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ORGANISM: TPRP-F1 GENOMIC CLONE
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                       TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8241 ATTIGGAAGAACTCTTAAATCTCTAAATGATCTTGTTGATAAATATCAAAAACAAATCG 8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8181 AAGAAATTACAAAACAAATTGATTTTATCAAAAAAGTTGATGAAACTTTTAAACAAGAGA 8240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INCORNATION:
APPLICANT: BARG, Rivka
APPLICANT: BARG, Rivka
APPLICANT: BARG, Rivka
APPLICANT: SALTS, Thehiam
TITLE OF INVENTION: METHOD FOR THE INTRODUCTION OF GENETIC PARTHENOCARPY IN
TITLE OF INVENTION: PLANTS
FILE REPERENCE: INTRO GENETIC PARTHENOCAPRI IN PLANTS
CURRENT APPLICATION NUMBER: US/09/125,287B
CURRENT FILING DATE: 1998-11-09
EARLIER APPLICATION NUMBER: PCT/IL97/00051
BARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 CAGCTACAGGAAGAGTCCGTGTTTTAGAAGAACAGCTTGTTAAGGCCAAAGAACAGATTG 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 AAGACTIGAGGAGAAIGGCIGAGICTCCCGAAIACCAGAAGGCCCTAITGAICAGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      392 AAAATTACAAGAAACAAGCTAGGAATGATCTGGGAAAGGATCATGAAATCTTAAGG 447
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 36.8; DB 4; Length 12127; 50.6%; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
COMPUTER: HP VECTRA 486/33
COPERATING SYSTEM: MSDOS VERSION 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                        ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PB340P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09125287B
Patent No. 6114602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 12127 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
  Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                             STATE: Maryland
                                                                                                                                                                                                          20850
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LENGTH: 12839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-961-527-148
                                                                                                                                                                                     COUNTRY:
  APPLICANT:
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1586 TCTACTATTTTGGAGGCCAAAATGCCCACAACCAGATTGCAGTTTATCCTCACCAACCTC 1645
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                                                                                                                                                                                                                                                      DB 3; Length 12839;
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                                                                                                                             1.8%; Score 36.2; DB 3;
22.5%; Pred. No. 4.6;
tive 67; Mismatches 102;
FEATURE:
NAME/KEY: unsure
LOCATION: (5)..(11322)
OTHER INFORMATION: "n"'8 are any nucleic residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: February 2, 2004, 18:41:04 Job time: 152.431 secs
                                                                                                                                                       Best Local Similarity 22.5
Matches 49; Conservative
                                                                                     US-09-125-287-1
                                                                                                                                    Query Match
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(without alignments)
10417.799 Million cell updates/sec
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1: \( \text{cgn2} \) \( \text{fptodata} \) \( 1 \text{pubpa} \) \( \text{VUBCOMB} \) \( \text{seq} : * \)

2: \( \text{cgn2} \) \( \text{fptodata} \) \( 1 \text{pubpa} \) \( \text{PUBCOMB} \) \( \text{seq} : * \)

3: \( \text{cgn2} \) \( \text{fptodata} \) \( 1 \text{pubpa} \) \( \text{PUBCOMB} \) \( \text{seq} : * \)

4: \( \text{cgn2} \) \( \text{fptodata} \) \( 1 \text{pubpa} \) \( \text{VUS} \) \( \text{PUBCOMB} \) \( \text{seq} : * \)

5: \( \text{cgn2} \) \( \text{fptodata} \) \( 1 \text{pubpa} \) \( \text{VUS} \) \( \text{PUBCOMB} \) \( \text{seq} : * \)

6: \( \text{cgn2} \) \( \text{fptodata} \) \( 1 \text{pubpa} \) \( \text{VUS} \) \( \text{PUBCOMB} \) \( \text{seq} : * \)

7: \( \text{cgn2} \) \( \text{fptodata} \) \( 1 \text{pubpa} \) \( \text{VUSO} \) \( \text{PUBCOMB} \) \( \text{seq} : * \)

9: \( \text{cgn2} \) \( \text{fptodata} \) \( 1 \text{pubpa} \) \( \text{VUSO} \) \( \text{PUBCOMB} \) \( \text{seq} : * \)

10: \( \text{cgn2} \) \( \text{fptodata} \) \( 1 \text{pubpa} \) \( \text{VUSO} \) \( \text{PUBCOMB} \) \( \text{seq} : * \)

11: \( \text{cgn2} \) \( \text{fptodata} \) \( 1 \text{pubpa} \) \( \text{VUSO} \) \( \text{PUBCOMB} \) \( \text{seq} : * \)

12: \( \text{cgn2} \) \( \text{fptodata} \) \( 1 \text{pubpa} \) \( \text{VUSO} \) \
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6/ptodata/1/pubpna/US10_NEW_PUB.seq:
6/ptodata/1/pubpna/US60_NEW_PUB.seq:
6/ptodata/1/pubpna/US60_PUBCOMB.seq:
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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2008
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		Description	Sequence 1, Appli	Sequence 2, Appli	Sequence 381, App	Seguence 9, Appli	Seguence 1, Appli	Sequence 6, Appli	Sequence 7, Appli	Sequence 33468, A	Sequence 3, Appli	Sequence 13359, A	Sequence 13292, A	Sequence 18181, A	Sequence 30284, A	Sequence 274, App	Sequence 1421, Ap
		QI	US-09-971-773-1	US-09-971-773-2	US-10-106-698-381	US-09-839-136-9	US-09-839-136-1	US-09-971-773-6	US-09-971-773-7	US-09-918-995-33468	US-09-971-773-3	US-09-864-761-13359	US-09-864-761-13292	US-09-864-761-18181	US-09-864-761-30284	US-10-125-968-274	US-09-864-761-1421
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		Query Match	100.0	78.9	78.4	78.2	73.3	48.6	44.5	18.3	15.0	14.2	10.9	10.6	10.6	7.4	6.8
		Score	2008	1584	1574.2	1569.6	1472.6	976.4	893.2	368.2	302	285.6	218.8	213.4	213.4	149	136.4
		Result No.	-	7	m	4	2	9	7	8	6	10	11	12	13	14	15

Sequence 52289, A Sequence 33106, A Sequence 23971, A Sequence 23971, A Sequence 218, App Sequence 518, App Sequence 518, App Sequence 3140, App Sequence 1390, App Sequence 1390, App Sequence 1390, App Sequence 96, App Sequence	
US-10-242-535A-52289 US-09-918-995-33106 US-09-908-975-23971 US-09-908-975-23971 US-09-908-975-23971 US-09-908-975-23971 US-09-908-975-4992 US-10-184-644-518 US-10-312-841-2 US-09-764-891-840 US-09-764-891-840 US-10-274-450-18 US-10-274-450-18 US-10-10-27-450-18 US-10-140-472-96 US-10-140-865-96 US-10-141-759-96	
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## ALIGNMENTS

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                                                                                                                       APPLICANT: Kazuwasu NAKAMURA
APPLICANT: Kazuwasu NAKAMURA
APPLICANT: Kazuwasu UGHIDA
APPLICANT: Toyohida SHINKAWA
APPLICANT: Toyohida SHINKAWA
APPLICANT: Toyohida SHINKAWA
APPLICANT: Motoo YAMASKI
APPLICANT: Motoo YAMASKI
APPLICANT: Motoo YAMASKI
APPLICANT: NO. US20030115614Aluo HANAI
ITILE OF INVERTION: ANTIBODY COMPOSITION-PRODUCING CELL
FILE REFERENCE: 249-202
CURRENT APPLICATION NUMBER: US/09/971,773
CURRENT FILING DATE: 2002-08-30
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-06
PRIOR FILING DATE: 2001-06
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 10.
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Sequence 1, Application US/09971773 Publication No. US20030115614A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 2008; Conservative
                                                                                                            Mitsuo SATOH
                                                                            APPLICANT: Yutaka KANDA
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1 AACAGAAACTTATTTTCCTGTGGGCTAACTAGAACCAGAGTACAATGTTTCCAATTCTT 60

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Gaps

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US-10-106-698-381

Sequence 381, Application US/10106698

Sequence 381, Application US/10106698

Publication No. US20030109690A1

GENERAL INFORMATION:
TITLE REFERENCE: PA005P1

FILE REFERENCE: PA005P1

CURRENT APPLICATION UNMBER: US/10/106,698

CURRENT FILING DATE: 2002-03-27
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                                                                                                                                                Length 1728;
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FILE REFERENCE: 249-202
CURRENT APPLICATION NUMBER: US/09/971,773
CURRENT FILING DATE: 2002-08-30
FRIOR APPLICATION NUMBER: UP 2000-308526
FRIOR FILING DATE: 2000-10-06
FRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO. 1779
                                                                                                                                                Score 1584;
Pred. No. 0;
                                                                                                                                              78.9%;
94.8%;
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Matches 1638; Conservative
                                                                                                          TYPE: DNA
CRGANISM: Mus musculus
US-09-971-773-2
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PRIOR APPLICATION NUMBER: PCT/USO0/26524
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR APPLICATION NUMBER: US 60/163,280
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 381
LENGTH: 3007
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (2984)
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US-09-839-136-1
; Sequence 1, Application US/09839136
; Patent No. US20020081694A1
; GENERAL INFORMATION:
; APPLICANT: NAOYUKI TANIGUCHI et al.
; TITLE OF INVENTYON: ALPHA 1-6 FUCOSYLTRANSFERASE
; FILE REFERENCE: 2356-7
; CURRENT APPLICATION NUMBER: US/08/839,136
; CURRENT FILING DATE: 2001-04-23
; PRIOR FILING DATE: 1999-11-18
; PRIOR FILING DATE: 1998-01-07
; STORTWARE: FSEQ ID NOS: 15
; SOFTWARE: FSEQ ID NOS: 15
; SEQ ID NO 1-07
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US-09-839-136-1
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NAME/KEY: CDS
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ORGANISM: Pig
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; Sequence 7, Application US/09971773; Publication No. US20030115614A1; GENERAL INFORMATION:
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US-09-971-773-7
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Sequence 6, Application US/09971773
Publication No. US20030115614A1
GENERAL INFORMATION:
APPLICANT: Witaka KANDA
APPLICANT: Razubias UGHIDA
APPLICANT: Razubias UGHIDA
APPLICANT: No. US20030115614A1uo HANAI
APPLICANTON: NUMBER: US/09/971,773
CURRENT APPLICATION NUMBER: US 60/268,926
PRIOR PILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PATENTIN Ver. 2.1
IENGTH: BANGHI NOS: 73
IENGTH: BANGHI NOS: 73
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88.6%; Score 976.4; DB 11;
Best Local Similarity 99.9%; Pred. No. 3.4e-273;
Matches 977; Conservative 0; Mismatches 1;
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US-09-971-773-6
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APPLICANT: Yutaka KANDA
APPLICANT: Mitsuo SATOH
APPLICANT: Kazuyasu NAKAMURA
APPLICANT: Kazuyasu NAKAMURA
APPLICANT: Kazuyasu NAKAMURA
APPLICANT: Toyohide SHINKAWA
APPLICANT: Naoko YAMANI
APPLICANT: Naoko YAMANI
APPLICANT: No. US20030115614Aluo HANAI
TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL
TITLE OF INVENTION ANTIBODY COMPOSITION-PRODUCING CELL
TITLE OF INVENTION NUMBER: US/09/971,773
CURRENT FILING DATE: 2002-08-30
FRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/268,926
PRIOR FILING DATE: 2001-0-16
PRIOR APPLICATION NUMBER: US 60/268,926
PRIOR APPLICATION NUMBER: US 60/268,926
PRIOR PELING DATE: 2010-0-10-06
PRIOR APPLICATION NUMBER: US 60/268,926
PRIOR APPLICATION NUMBER: US 60/268,926
PRIOR APPLICATION NUMBER: 2010-0-16
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Pred. No. 5.8e-249;
0; Mismatches 53;
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Best Local Similarity 94.6%;
Matches 925; Conservative
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; ORGANISM: Rattus norvegicus
US-09-971-773-7
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1598 1658 1718 1719 TAAAGGTGTCAACAGAAAACTAGGAAAAACAGGCCTGTACCTTCCTACAAAGTCCGAGA 1778 1162 ö 1043 GACTCCTGAGGTCCATGGTGATCCTGCAGTGGGTGGTATCCCAGTTTGTCAAATACT 1102 1163 TCAAACATCCAGTTATTGGAGTCCATGTCAGACGCACTGACAAAGTGGGAACAGAAGCAG 1222 840 983 ACAGCCTCCATCCTCGTCCTCCTTACTTACCCTTGGCTGTACCAGAAGACCTTGCAGATC 1042 960 982 121 181 301 241 TCAAACATCCAGTTATTGGAGTCCATGTCAGACGCACAGACAAAGTGGGAACAGAAGTG 361 61 62 GACACTGGTCAGGTGAAGTGAAGGACAAAAATGTTCAAGTGGTCGAGCTTCCCATTGTAG 242 TGATCCGCCCACAGGCTTGGCTAGAAAAAGAAATAGAAGAAGCCACCACCAAGAAGCTTGGCT AGGCCAAAATGCCCACAACCAGATTGCAGTTTATCCTCACCAACCTCGAACTAAAGAGGA 1659 AATCCCCATGGAACCTGGAGATATCATTGGTGGCTGGAAACCATTGGAATGGTTACTC 841 AATTCCAATGGAACCTGGAGATATCATTGGTGTGGCTGGAAACCATTGGGATGGTTATTC 923 GACACTGGTCAGGTGAAGTGAAGGACAAAAATGTTCAAGTGGTCGAGCTCCCCATTGTAG 182 GACTIGIACGAGIGCAIGGIGACCIGCAGIGIGGGGGGGGIGICTCAGITIGICAAATACT TGATCCGTCCACACCTTGGCTGGAAAGGGAAATAGAAGAAACCACCAAGAAGCTTGGCT Gaps ö DB 11; Length 422; 33; Indels OBTAINED Sequence 33468, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: Hyeeq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT.

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT PELLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR SEQ ID NOS: 38054

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 33468 Score 368.2; DB 1 Pred. No. 2.5e-96; 0; Mismatches 33 1779 GAAGATAGAAACAGTCAA 1796 18.3%; 92.2%; Query Match
Best Local Similarity 92.2
Matches 388; Conservative ; ORGANISM: Homo sapiens US-09-918-995-33468

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362 ccriccarcccarreaagagracargerecarcrrcaagaacarrreagcrrcrrecac 421
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                                                                                                                                                                                                                                                                                               APPLICANT: Nacko YAMANE
APPLICANT: Nacko YAMANE
APPLICANT: Motoo YAMASAKI
APPLICANT: No. US20030115614Aluo HANAI
TITLE ON INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL
FILE REFERRNCE: 249-202
CURRENT APPLICATION NUMBER: US/09/971,773
CURRENT FILING DATE: 2000-006
PRIOR PILING DATE: 2000-006
PRIOR PLILING DATE: 2000-106
PRIOR PLILING DATE: 2000-10-06
PRIOR PLILING DATE: 2001-02-16
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3.3e-76;
hes 0;
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                                                                                                                                                         Sequence 3, Application US/09971773
Publication No. US20030115614A1
GENERAL INFORMATION:
APPLICANT: Yutaka KANDA
                                                                                                                                                                                                                             Mitsuo SATOH
Kazuyasu NAKAMURA
Kazuhisa UCHIDA
Toyohide SHINKAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Cricetulus griseus
US-09-971-773-3
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SEQ ID NO 3
LENGTH: 9196
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US-09-864-761-13359
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APPLICANT:
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Sequence 13359, Application US/09864761 Patent No. US20020048763A1

GENERAL INFORMATION: APPLICANT: Penn, Sharron G.

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APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Weshbergy
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMBER: US/09/864.761
CURRENT APPLICATION NUMBER: US/09/864.761
CURRENT PILING DATE: 2001-05.246
PRIOR APPLICATION NUMBER: US 60/180.312
PRIOR APPLICATION NUMBER: US 60/20.366
PRIOR PLING DATE: 2000-06.32
PRIOR PLING DATE: 2000-06.32
PRIOR PLILING DATE: 2000-01-07
PRIOR PLILING DATE: 2001-01-07
PRIOR PLILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
OTHER PROPAGATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
US-09-864-761-13359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 285.6; DB 9;
Pred. No. 3.2e-72;
0; Mismatches 54;
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Best Local Similarity 85.5
Matches 318; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1505
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APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: HUMAN GENOME EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-06-26
PRIOR PELING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                992 ATCCTCGTCCTCATTACTTACCTTGGCTGTACCAGAAGACCTTGCAGATCGACTCCTGA 1051
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                                                                                                                                                                                                                                                                                                                      872 TGTTTAGACCTGTAAGTGAGACATGCACAGACAGGTCTGGCCTCTCCACTGGACACTGGT
                                                                                                                                                                                                                                             ö
                                                                                                                                                                           Length 551;
                                                                                                                                                                                                                                                Indels
; OTHER INFORMATION: MAP TO AL109847.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
US-09-864-761-13292
                                                                                                                                                                    Score 218.8; DB 9;
Pred. No. 9.5e-53;
0; Mismatches 57;
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PRIOR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
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Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
                                                                                                                                                                       Query Match 10.9%;
Best Local Similarity 81.6%;
Matches 253; Conservative 0
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Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: HANDAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENOME SERRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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                                        245
                                                                                                                                                                               246 GGACGGCCTATATCCCTCCTACAAGTTCGAGAGAGATAGAAACGGTCAAGTACCCCA 305
                                                                                                                                                                                                                                                                                                                      306 CATATCCTGAGGCTGAGAATAAAGCTCAGATGGAAGAGATAAACGACCAAACTCAGTTC 365
                                                                                                                                                                                                                                                    CATATCCTGAAGCTGAAAATAGAGATGGAGTGTAAGAGTTAACAACAGAATTTAGTTC
                                        186 TTGGTGGCTGGAAATCATTGGGATGGCTATTCTAAAGGTGTCAACAGGAAATTGGGAA
                                                                                                             1745 AAACAGGCCTGTACCCTTCCTACAAAGTCCGAGAAGATAGAAACAGTCAAATACCCTA
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 13292
LENGTH: 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCES. ACOUNTER. 18, 900 CONTENT APPLICATION NUMBER: US/09/864,761 CURRENT APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2001-05-23 PRIOR FILING DATE: 2000-02-04 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-08-03 PRIOR FILING DATE: 2000-08-03 PRIOR FILING DATE: 2000-09-03 PRIOR APPLICATION NUMBER: US 60/236,359 PRIOR FILING DATE: 2001-01-30 PRIOR FILING DATE: 2001-01-30 PRIOR PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00669 PRIOR FILING DATE: 2001-01-30 PRIOR FILING DATE: 2001-01-30 PRIOR PRIOR FILING DATE: 2001-01-30 PRIOR PRIOR FILING DATE: 2001-01-30 PRIOR FILING DATE: 2001-01-20 PRIOR FILING DATE: 2001-01-2
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US-09-864-761-13292
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1115 AACCTTGGCTGGAAAGGGAAATAGAAGAAACCACCAAGAAGCTTGGCTTCAAACATCCAG 1174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: MAP TO ALL09847.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: SWISSPROT HIT: G9VLZ7, EVALUE 6.50e+00
OTHER INFORMATION: EGT HUMAN HIT: AM387766.1, EVALUE 0.00e+00
OTHER INFORMATION: NT HIT: AF038280.1, EVALUE 0.00e+00
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                      PRIOR PLING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PLING DATE: 2000-08-03
PRIOR PLING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,356
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-09-27
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-20
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Matches 226; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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SEQ ID NO 30284
LENGTH: 248
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Sequence 30284, Application US/09864761

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: How Wensheng

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REPERBUGE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT PILLING DATE: 2001-05-23
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OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4.2

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN PEACENTA, SIGNAL = 3.6

OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 3.6

OTHER INFORMATION: EXPRESSED IN HERRY, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN HERRY, SIGNAL = 5.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 10.6%; Score 213.4; DB 9; Length Best Local Similarity 91.5%; Pred. No. 2.1e-51; Matches 226; Conservative 0; Mismatches 21; Indels
                      PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 18181
2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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PRIOR FILING DATE:
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US-09-864-761-30284
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992 ATCCTCGTCCTCCTTACCTTGCCTGTACCAGAAGACCTTGCAGATCGACTCCTGA 1051
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N: EXPRESSED IN BT474, SIGNAL = 4.2

N: EXPRESSED IN FETAL LIVER, SIGNAL = 3.5

N: EXPRESSED IN PEACENTA, SIGNAL = 4.6

N: EXPRESSED IN HEAL100, SIGNAL = 3.6

N: EXPRESSED IN HEART, SIGNAL = 3.5

N: EXPRESSED IN UNG, SIGNAL = 5.1

N: EXPRESSED IN ADMIN, SIGNAL = 5.1

N: EXPRESSED IN ADMIT, LIVER, SIGNAL = 2.7

N: EXPRESSED IN HELA, SIGNAL = 3.3

N: EXPRESSED IN HELA, SIGNAL = 2.7

N: EXPRESSED IN BONE MARROW, SIGNAL = 2.9
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Best Local Similarity 76.6%; Pred. No. 7.4e-29;
Matches 167; Conservative 0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 1421
LENGTH: 384
             PRIOR PLING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-08-03
PRIOR PLING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,356
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
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ORGANISM: HOMO SADIENS
FEATURE:
OTHER INFORMATION: MAP TO ALL09.
OTHER INFORMATION: EXPRESSED IN
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Sequence 1421, Application US/09864761
Sequence 1421, Application US/09864761
Sequence 1421, Application US/09864761
Sequence 1421, Application US/09864761
Sexuence 1421, Application Sharron G.
APPLICANT: Penn, Bank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                           APPLICANT: Palermo, Adam
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
APPLICANT: Steinmann, Kathleen
APPLICANT: Steinmann, Kathleen
APPLICANT: Blias, Josh
APPLICANT: Blias, Josh
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: WHENER: US/10/125,968
CURRENT APPLICATION NUMBER: US/10/125,968
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,163
PRIOR APPLICATION NUMBER: US 60/285,163
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 TACAAGAAAACAGACCAGTAAATGGTCTGGGGAAGGATCATGAAATCCTGAGGAGGAGGA 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           455 TTGAAAATGGAGCTAAAGAGCTCTGGTTTTTTTTTAAAGTGAATTGAAGAAATTAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature; LOCATION: 204, 266, 320, 328, 402, 424, 462, 470; OTHER INFORMATION: n = A,T,C or G US-10-125-968-274
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                    Sequence 274, Application US/10125968 Publication No. US20030215805A1 GENERAL INFORMATION: APPLICANT: Lillie, James
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ORGANISM: Homo sapiens
241 TTATTGG 247
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ENGTH: 481
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Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230003K17 product:fucosyltransferase 8, AK051811 AK051811 GI:26342229
MHTC; CAP trapper.
                                                                                   AUZ4128 AU124128
BU513162 AGENCOURT
EN5414472 EN414472
CB989769 AGENCOURT
BO60458 MI -P - CPI-
E154634 6 60318 8856
CB105621 K - EST0130
CB105621 A CENCOURT
BC952954 H4019B10-
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CB105910 K - EST0135
BC4539475 CC279D08-
CB105910 K - EST0130
BC771085 602719363
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          BX452321 BX452321
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BX429921 BX429921
BX450010 BX450010
BU184296 AGENCOURT
CB194828 AGENCOURT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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                                                                                                    BU513162
BB(41472
BB(604588)
BQ(604588)
BD(604588)
BB1546364
CB105621
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CB194828
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Mus musculus
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ACCESSION
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ORGANISM
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AUTHORS
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             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1809.4
831.6
810
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Minimum DB Maximum DB

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LIRPOPWLEKEIEBATKKLGFKHPVIGVHYRRTDKYGTEAAFHPIESYWHYBEHFQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LARRAQUDKKRVYLATDDPTLLKEAKTKYSNYBFISDNSISWSAGLHNRYTENSLRGV
ILDIHFLSQADFLVCTFSSQVCRVAYEIMQTLHPDASANFHSLDDIYYFGGQNAHNQI
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/dev stage="12 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359 AAGAACAGCTTGTTAAGGCCAAAGAACAGATTGAAAATTACAAGAAACAAGCTAGGAATG 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTTTTTTCTACAAAGTGAATTGAAGAAATTAAAGAAATTAGAAGGAAACGAACTCCAAA 538
                                                                                                                                                                                                                                                                                                                                                /note="unnamed protein product; fucosyltransferase 8 (MGD|MG1:1858901, GB|NM_016893, evidence: BLASTN, 99%, match=2175)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCATTTGGTTCGAGATAATGACCACCTGATCACTCCAGCAGAGAACTCTCCAAGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419 ATCTGGGAAAGGATCATGAAATCTTAAGGAGGAGGATTGAAAATGGAGGTAAAGAGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 AAAAGAAACCIATTTTCTTGTGTGGCTAACTAGAACCAGAGTACAATGTTTCCAGTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCATTTGGTTCGAGATAATGACCACCCTGACCATTCTAGCAGAGAACTCTCCAAGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        612 TTGCAAAGCTTGAACGCTTAAAACAGCAAAATGAAGACTTGAGGCGAATGGCTGAGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 TCCGAATACCAGAAGGCCCTATTGATCAGGGGACAGCTACAGGAAGAGTCCGTGTTTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                672 recenaraceagandececentranceagadancageracagangagereceretrang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AACAGAAACTTATTTTCCTGTGTGGCTAACTAGAACCAGAGTACAATGTTTCCAATTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TGAGCTCCGAGAAGACAGA--AGGGAGTTGAAACTCTGAAAATGCGGGCATGGACTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 CCTGGCGTTGGATTATGCTCATTCTTTTTGCCTGGGGGACCTTATTGTTTTATATAGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.1%; Score 1809.4; DB 11; Length 2766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0;
0; Mismatches 116; Indels
                                                                                                                               /db_xref="FANTOM_DB:D230003K17"
/db_xref="taxon:10090"
                                     organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        b
                                                                 mol_type="mRNA"
'strain="C57BL/6J"
                                                                                                                                                                                                /clone="D230003K17"
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Skonno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamancto, R., Matsunico, H., Sakaguchi, S., Itegami, T., Rashimagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer General General
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-ULI-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Analysis of the mouse transcriptome based on functional annotation of 60,70 full-length cDNAs
Nature 420, 563-573 (2002)
( (bases 1 to 2766)
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Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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1932   CTGCGAACTTCCATTCTTGGATGACATCTATTTTGGAGGCCA   1619   AGATTGCAGTTTATCCTCACCAACCTCGAACTAAAGAGGAAATTCC   1952   AGATTGCTGTTTATCCTCACAAACCTCGAACTGAAGAGGGAAATTCC   1679   ATATCATTGGTGTGGCTGGAAACCATTGGAATGGTTACTCTAAAGG   1730   ATATCATTGGTGTGGCTGGAAACCATTGGAATGGTTACTCTAAAGG   1731   TAGGAAAAACGGCTGGAAACCATTGGAATGGTTATTCTAAAGG   1731   TAGGAAAAACGGCTGTACCCTTCCTACAAGTCCGAGGAAGAT   1732   TAGGAAAAACAGGCTGTACCCTTCCTACAAGTCCGAGAAGAT   1733   TAGGAAAAACAGGCTGAAACTCCTACAAGTCCGAGAAGAT   1734   ATGCTCACACTTCTGAGCTGAAAATAGAGATGGTGAAAGAAA	AK048520  AK048520  Mas musculus 16 days embryo head cDNA, RIKEN full library, clone:C1:0068P22 product:fucosyltransfe sequence.  AK048520  AK048520  HTC; CAP trapper.  Mus musculus  Mus musculus (house mouse)  Mus musculus  Relatovota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Rodentia; Sciurognathi; Muril Ligh-efficiency full-length cDNA cloning  Meth. Elexamol. 303, 19-44 (1999)  S 20499353  10496366  Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y. Ich, M., Konno, H., Okazaki, Y., Muramatsu, M. and Normalization and subtraction of cap-trapper-selpscaper full-length cDNA libraries for rapid dis Genome Res. 10 (10), 1617-1630 (2000)  20499374  S Shibata, K., Itch, M., Akiyama, J., Nishi, K., Kiteunai, T., Tas Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tas Sumi, N. Ishii, Y., Makamura, S., Hazama, M., Nishii, Y. Wamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikanawa, Yoneda, Y., Ishikawa, T., Ozawa, K., Tanawa, T., Matsumoto, R., Matsumoto, H., Sakaguchi, S., Ikanawa, Yoneda, Y., Ishikawa, T., Ozawa, K., Tanawa, T., Matsumoto, R., Matsumoto, H., Sakaguchi, S., Ikanawa, Yoneda, Y., Ishikawa, T., Ozawa, K., Tanawa, T., Matsumoto, H., Sakaguchi, S., Ikanawa, Yoneda, Y., Ishikawa, T., Ozawa, K., Tanawa, T., Matsumoto, H., Sakaguchi, S., Ikanawa, Yoneda, Y., Ishikawa, H., Inoue, Y., Kita, A. and RIKEN integrated sequence analysis (RISA) system sequencing pipeline with 384 multicapillary sequencence analysis (RISA) system sequencing pipeline with 384 multicapillary squageneral saccione Res. 10 (11), 1757-1771 (2000)  11076861  S Kawai, J., Yonhagawa, A., Shibata, K., Yoshino, M., Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M.,
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Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Salto, T., Okazaki, Y., Gojobori, T., Bondo, S., Yamanaka, I., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Fletcher, C., Fujita, M., Garibold, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ranyalad, M., Rodriguez, T., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wanshi, S., Schollad, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
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Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 3052)
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(MGD|MG1:1858901, GB|NM_016893, evidence: BLASTN, 99%,
match=2175)
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Nature 409 (6821), 685-690 (2001)
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pcMV-seporfe.lccdb; Site l: BcoRV; Site 2: Not1; Cloned
unidirectionally. Primer: Oligo dr. Average insert size
2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this
is a NIH MGC liberary."
215 C 209 g 244 t l others
                                                                                                                                                                                                                                                                                                                                   937 bp mRNA linear EST 16-AUG-2002
5', mRNA sequence.
BQ892101
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Susan L. Sullivan, PhD.

CDNA Library Preparation: ResGen, Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: WGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llh.gov

Plate: LLAM13875 row: d column: 14

High quality sequence start: 130

High quality sequence start: 130

High quality sequence stop: 780.

Location/Qualifiers

I. 937
ATCCCACATATCCTGAAGCTGAAAATAGAGATGAAGTAGAAGAGGATAACAACAGAACT
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                                                                                   2413 CACTICAGACCATCTKGGCCAGAGCAGAAGACGCAGACTAACACGTGGTTCATIGATAGACAC
                                                              TAGTTCAGACCATCTCAGCCAAGCAGAAGACCCAGACTAACATATGGTTCATTGACAGAC
                                                                                                                                             1919 ATGCTCCGCACCAAGAGCAAGTGGGAACCCTCAGATGCTGCACTGGTGGAACGCCTCTTT
                                                                                                                                                               ACGCTCCACACCAAGAGCAAGCGGAACCCTCAGATGCTGCACTGGTGGAACGCCTCTTT
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 3.9e-187;
0; Mismatches 55; Indels 1;
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Mus musculus
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llarity 94.0%;
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                          CCAGGAAGCTGGTGTGTAAAACATCAATAAAGGCTGTGGGCTATGGTTGTCAACTCCATCACG
                                                                                                         ATTGGCGCTATGCTACTGGTGGATGGACATGTTTTAGACCTGTAAGTGAGACATGTA
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        CCAGAAAGCTGGTATGTAATATCAACAAAGGCTGTGGGCTATGGATGTCAACTCCATCATG
                                                                                     TGGTTTACTGCTTCATGATTGCTTATGGCACCCCAGCGAACACTCATCTTGGAATCTCAGA
                                                                                                                                                                 ATTGGCGCTATGCTACTGGAGGATGGGAGACTGTGTTTAGACCTGTAAGTGAGACATGCA
                                                                                                                                                                                                                                                CAGACAGGTCTGGCCTCTCCACTGGACACTGGTCAGGTGAAGTGAAGGACAAAATGTTC
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Email: cgapbe-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bisscience Corporation
Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2025 row: p column: 07
High quality sequence stop: 666.
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Pred. No. 5.7e-182;
0; Mismatches 89;
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/clone="IMAGE:5798262"
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Best Local Similarity 90.7
Matches 894; Conservative
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1 (bases 1 to 1066)
NIH-MGC http://mgc.nci.nih.gov/.
NiH-MGC http://mgc.nci.nih.gov/.
Unpublished
Unpublished
Contact: Robert Strausberg, Ph.D.
    ATTCAAGTGGTCGAGCTCCCCATTGTAGACAGCCTCCATCCTCGGCCTCCTTACCTA
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Pred. No. 5.6e-172;
0; Mismatches 70;
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92.0%;
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/tissue_type="hepatocellular carcinoma, cell line"
/tissue_type="hepatocellular carcinoma, cell line"
/tish host="billo by page-resistant"
/clone_lib="NIH MGC_loop"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2: BCORI; CDNA made by oligo-dT priming. Directionally cloned into EccnI/XhoI sites using the following 5: adaptor: GGCACCAG(G): Site_selected >500bp for average insert site l: 8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 940)
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Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2445 row: k column: 03

High quality sequence stop: 700.
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     541 ATATTTACCCTTGGCTGTACCAGAAGACCTCGCAGATCGACTTGTACGAGTGCATGGTGA
                                        1065 TCCTGCAGTGTGGGTATCCCAGTTTGTCAAATACTTGATCCGTCCACAACCTTGGCT
                                                             601 CCCTGCAGTGTGGGGGTGTCTCAGTTTGTCAAATACTTGATCCGCCCACAGCCTTGGCT
                                                                                                                 GGAAAGGGAAATAGAAGAAACCACCAAGAAGCTTGGCTTCAAACATCCAGTTATTGGAGT
                                                                                                                                                     661 AGAAANAGAAATAGAAGAAGCCACCAAGAAGCTTGGCTTCAAACATCCAGTTATTGGAGT
                                                                                                                                                                                          CCATGTCAGACGCACTGACAAGTGGGAACAGAAGCAGCCTTCCATCCCATTGAGGAATA
                                                                                                                                                                                                                         721 CCATGICAGACGCACAGACAAGIGGGGACAGAAGCIGCCIICCAICCCAIIGAAGAGIA
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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/mol_type="mRNA"
/db xref="taxon:9606"
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/tissue_type="melanotic melanoma"
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//organism="Homo sapiens"
//db_xref="manAn"
//db_xref="taxon:9606"
//clone="CostorOsy007"
//clone="Vector Scale Line"
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                                                                           900 bp mRNA linear EST 22-MAY-200
BX452321 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA
clone CSODG005YO07 5-FRIME, mRNA sequence.
BX452321
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1 (bases 1 to 900)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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BP 191 91006 EVRY cedex - France
Bmail: sequenscope.cns.fr, web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7499.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAG023ZH04 CS02144_1&cluster=7499.f.
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://tulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAG023ZH04_CS02144_1.
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                                                                                                                                                                                                                BX452321.1 GI:31026371
                                                                                                                                                                                                                                                                 Homo sapiens (human)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information cloud through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM13505 row: e column: 17
High quality sequence stop: 641.
                                                                     1222 GCCTTCCATCCCATTGAGGAATACATGGTACACGTTGAAGAACATTTTCAGCTTCTCGAA
                                                                                                                                                                494 GCCTTCCATCCATTGAAGAGTACATGGTGCATGTTGAAGAACATTTTCAGCTTCTTGCA
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  374 TTGATCCGCCCACAGCCTTGGCTAGAAAAGAATAGAAGAAGCCACCAAGAAGCTTGGC
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoi
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 886)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
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7
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                                                                                                             Score 751.2; DB 13;
Pred. No. 5.6e-168;
0; Mismatches 69;
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923 bp mRNA linear EST 15-MAY-2003
Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens CDNA
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7499.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.igi?seq=CSOBAA012ZA08 CS01114_l&cluster=7499.f.
Contact: Feng Liang Email: fliang@lifetech.com URL:
Contact: Feng Liang Email: fliang@lifetech.com URL:
Location.com Genoscope sequence ID: CSOBAA012ZA08_CS01114_1.
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Li,W B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
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11 Similarity 92.5%; Pred. No. 1.5e-165;
821; Conservative 0; Mismatches 63;
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Mammalia; Butheria; Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 1027)

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cgi-bin/cluster.cgi?seq=CSOASO09ZBOBQPl&cluster=7499.f. Contac
cgi-bin/cluster.cgi?seq=CSOASO09ZBOBQPl&cluster=7499.f. Contac
Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
http://fulllength.invitrogen.com/ InvitroGen Corporation
Faraday Avenue Genoscope sequence ID : CSOASO09ZBOBQPI.
Location/Qualifiers
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Genoscope - Centre National de Sequencage
BE 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7499.f
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/mol_type="mRNRA"
/db_xref="taxon:9606"
/clone="CS0DG005Y007"
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/cell line="RAMOS CELL LINE"
/clone lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="Veccor: pCWVSORT G; lst strand cDNA was primed
with a Not1-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned
the Not I and EcoRV sites of the pCMVSPORT G vector.
Library was normalized."
9 others
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/organism="Mus musculus"
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/db_xref="taxon:10090"
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/tissue_type="retinoblastoma"
/tissue_type="retinoblastoma"
/tish_bogt="DH10B (phage-resistant)"
/clone_lib="NHH MGC 67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
                                                          855 bp mRNA linear EST 04-SEP-2002
-7971158 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6171012
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 855)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: ATC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can by
ttp://image.llnl.gov
http://image.llnl.gov
Plate: LLAMI3538 row: k column: 13
High quality sequence stop: 711.
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36.8%; Score 738; DB
Best Local Similarity 92.2%; Pred. No. 7.7e-
Matches 777; Conservative 0; Mismatches
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/mol_type="mRNA"
/db xref="taxon:9606"
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NIH-WGC http://mgc.nci.nih.gov/,
National Institutes of Health, Mammalian Gene Collection (WGC)
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Pregiaration: Invitrogen Corp
CDNA Library Pregiaration: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: NDAM0035 row: h column: 22
High quality sequence stop: 658.
                                                                                                               CCAAAAAGCTGGTGTAATATCAACAAAGGCTGTGGCTATGGCTGTCAGCTCCATCATG
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372 TATACTACCTCAGTCAGACAGATGGAGCAGGTGGTTGGCGGGAAAAGAGGGCCAAAGAC
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IMAGE:30136221 5', mRNA sequence.
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 135"
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Normalized full-length enriched library from pooled mous embryonic limb, maxilla and mandible, day 12.5, 13.5, 14 and 15.5 (size for the 0.5-1 kb fragments) cloned directionally, priming method: Oligo-dr. cDNA enrichment: >1k bp, Average insert size 1.6k bp. Normalization (cot value): 7.5 kb. Priming sequence: 5.GACTAGATCGCGAGCGGCCCC(T)3' Tissue contributed bavid Rowe. Library constructed by ResGen, Invitrogen
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                                                                                                                                                                                      DB 14; Length 898;
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                                                                                                                                                                                   Score 730.2; DB 14
Pred. No. 5.6e-163;
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                                                                                                                                                                                    Query Match
Best Local Similarity 93.4%;
Matches 784; Conservative
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AU124128 AVZRMZ Homo sapiens cDNA clone NT2RM2001714 5', mRNA sequence.
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Unpublished
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yama, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
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                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genomics@hri.co.jp
HRI human cDNA project; 5.- & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                         Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 ACATGGTGCATGTTGAAGAACATTTTCAGCTTCTTGCACGCAGAATGCAAGTGGACAAAA
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Catarrhini; Hominidae; Homo.
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Pred. No. 3.3e-153;
0; Mismatches 80;
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/cell_line="NT2"
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/db_xref="taxon:9606"
/clone="NT2RM2001714"
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 834)
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90.2%;
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Best Local Similarity 90.2
Matches 747; Conservative
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RESULT 12
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BX414472 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens CDNA clone CSODGO05YOO7 3-PRIME, mRNA sequence.
                                    Score 641.2; DB 13,
Pred. No. 9.2e-142;
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AGENCOURT 10116686 NIH_MGC_134 Mus musculus cDNA clone
IMAGE:6508154 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 937)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
cDNA Library Preparation: Invitrogen Corp
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLAMI4073 row: g column: 03
High quality sequence stop: 751.
                                                                                                                TCCTAGTGTGTACTTTTTCATCCCAGGTCTGTCGAGTTGCTTATGAAATTATGCAAACAC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mus musculus
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                                                                                                                                                                                                                                                                        GGCCTCTCCACTGGACACTGGTCAGGTGAAGTGAAGGACAAAAATGTTCAAGTGGTCGAG
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                                                                                                                                                                                TITGICAAATACTIGATCCGICCACAACCTIGGCIGGAAAAGGGAAATAGAAGAAACCACC
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                                            Gaps
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                                          72;
  937;
Length
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337 AGTTGCTTATGAAATTATGCAAACACTACATCCTGATGCCTCTGCAAACTTCCATTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30344717"
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/mol_type="MRNN"

/db_xrefe"taxon:9606"

/clone="CSODG005Y007"

/tissue type="B CELLS (RAMOS CELL LINE)"

/cell line="RAMOS CELL LINE"

/clone_libe="RAMOS CELL LINE"

/clone_libe="RAMOS CELL LINE"

/clone="Westor: pCMVSPORT 6; lst strand cDNA was primed

with a NotI-oligo(dT) primer. Five prime end enriched,

double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.

Library was not normalized."

library was 160 c 167 g 238 t lothers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1518 GGTTGCTTATGAAATCATGCAAACACTGCATCCTGATGCCTCTGCAAACTTCCATTCTTT 1577
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                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 757)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                       Conteact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 ENRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7499.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CSOBANO01ZF02 AN062 1&cluster=7499.f.
Contact: Feng Liang Email: fliang@lffetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBANO01ZF02_AN062_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             517 ATTAAAGGAGGCAAAAACAAAGTACCCCCAATTATTATTATTAGTGATAACTCTATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     457 CTGGTCAGCTGGACTGCACAATCGATACACAGAAAATTCACTTCGTGGAGTGATCCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1158 TGGCTTCAAACATCCAGTTATTGGAGTCCATGTCAGACGCACTGACAAAGTGGGAACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1218 AGCAGCCTTCCATTCCATTGAGGAATACATGGTACACGTTGAAGAACATTTTCAGCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        637 AGCTGCCTTCCATCCCATTGAAGAGTACATGGTGCATGTTGAAGAACATTTTCAGCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1278 CGAACGCAGAATGAAAGTGGATAAAAAAAAAGAGTGTATCTGGCCACTGATGACCCTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                577 TGCACGCAGAATGCAAGTGGACAAAAAAAGAGTGTATTTGGCCACAGATGACCCTTCTTT
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31.6%; Score 634.6; DB 13
Best Local Similarity 90.1%; Pred. No. 3.3e-140;
Matches 679; Conservative 0; Mismatches 75;
                            BX414472.1 GI:30653877
                                                                   Homo sapiens (human)
                                                                                        sapiens
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790 bp mRNA linear EST 01-MAY-2003
IMAGE:30344717 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-remail.nib.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninoi (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDRAM31 row h column: 06
High quality sequence stop: 619.
                                                                                                                                                                                                                                                                                                               1758 CCCTTCCTACAAAGTCCGAGAAGATAGAAACAGTCAAATACCCTACATATCCTGAAGC 1817
278
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 790)
                                                                                                                                    1638 CCAACCTCGAACTAAAGAGGAAATCCCCATGGAACCTGGAGATATCATTGGTGTGGGCTGG
                                                                                                                                                             217 CCAACCCCGAACTGCAGATGAAATTCCCCATGGAACCTGGAGATATCATTGGTGTGGCTGG
                                                                                                                                                                                                                                                                                                                                         1578 AGATGACATCTACTATTTTGGAGGCCAAAATGCCCACAACCAGATTGCAGTTTATCCTCA
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                                                                                                                                                                                                                                                                      157 AAATCATTGGGATGGCTATTCTAAAGGTGTCAACAGGAATTGGGAAGGACGGCCTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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GGCTGTACCAGAAGACCTTGCAGATCGACTCCTGAGAGTCCAT-GGTGATCCTGCAGTGT 1075
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                                                                                                                                                                                                                 CTGGTTTTTCCTACAGAGTGAATTGAAGAATTAAAGAACTTAGAAGGAAATGAACTCCA 206
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                                                                                                                                                                                                                                                                                  266
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                                                                                                                                                                                                                                                                                                                                                                                                           327 TCTGACAGAACTGGTTCAGCGGAGAATAACATATCTTCAGAATCCCAAGGACTGCAGCAA 386
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                                                                                            86
                                                                               TGATCTGGGAAAGGATCATGAAATCTTAAGGAGGAGGAGGATGAAAATGGAGCTAAAGAGCT
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                                                              357 AGAAGAACAGCTTGTTAAGGCCAAAGAACAGATTGAAAATTACAAGAAACAAGCTAGGAA
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                                 Gaps
                                 1;
   DB 14; Length 790;
Query Match 31.6%; Score 634.6; DB 14; Length Best Local Similarity 93.0%; Pred. No. 3.3e-140; Matches 675; Conservative 0; Mismatches 50; Indels
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Search completed: February 2, 2004, 18:36:52 Job time : 4338.69 secs THIS PAGE BLANK (USPTO)

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GenCore version 5.1.6
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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	February 2, 2004, 10:19:28; Search time 6342.17 Seconds (without alignments) 11146.322 Million cell updates/sec
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Database :	GenEmbl:* 1: gb_ba:*

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is the number of results predicted by chance to have a Pred. No.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	BD168517 Cells pro BC010666 Mus muscu BD168516 Cells pro AK662735 Sequence BD087745 Flant cel BD087745 Flant cel BD087745 Flant cel BD087745 Homo sapien K15725 Human mRNA AJ539536 Homo sapien X17977 Homo sapien X17977 Homo sapien X17977 Homo sapien X17977 Homo sapien X17978 Homo sapien AJ536054 Homo sapien AJ536054 Homo sapien AJ536058 Homo sapien AN5140707 Sequence E14720 Procine mRN BC622885 Homo sapi AJ514972 Procine mRN BC622885 Homo sapien AJ5149740 Homo sapien AJ514324 Homo sapien AJ51434 Homo sapien AJ51440477 Homo sapien AJ51434 Homo sapien AJ51434 Homo sapien AJ51440477 Homo sapien AJ51434 Homo sapien AJ51441	p DNA linear PAT 17-JAN-2003 sition.  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.  , Uchida, K., Shinkawa, T., Yamane, N., ai, N.
SUMMARIES	BD168517 BC01066 BC010666 BC010666 BC010666 BC010668516 BC0105198 BD0087745 BD09289 BE15725 BE15725 BE15725 BE15726 BE17720 BE	1728 b body compo 129 nouse) hordata; todentia; kkamura, K. 1, and Han
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661   GGTTGTCAACTCCAACAACTCCAACACTCATCATCATCATTCCTTATCCCTATTCCCAACACAACA	
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'lab host≈"DH10B"
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Butterfield, Y.S., Krzywinski, M.I., Schmutz, J., Myers, R.N.,
Butterfield, Y.S., Krzywinski, M.I., Salska, U., Smailus, D.E.,
Generation and mouse oDNA sequences
L. Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002)
                              BCU10666 Mus musculus fucosyltransferase 8, mRNA (cDNA clone MGC:11418 IMAGE:3594582), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Linn at: http://image.llnl.gov Series: IRAK Plate: 16 Row: 1 Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8393370.
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Nobisite: amg@bcm.tmc.edu
Gunatane, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 2976)
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Submitted (10-UTL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: Jeffrey Green M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
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1. .2976
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Email: cgapbs-r@mail.nih.gov
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Gaps

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RSIMTDLYYLSQTDGAGDWREKEAKDLTELVQRRITYLQNPROCSKARKLVCNINKGC
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ILDIHFLSQADFLVCTFSSQVCRVAYEIMQTLHPDASANFHSLDDIYYFGGGNANNQI
AVYPHKPRTEEEIPMFFGDIIGVAGNHWDGYSKGINRKLGKTGLYPSYKVREKIETVK
YPTYPEARF
                                  ROD 05-AUG-2000 complete cds.
                                                                                                                                                                                                                                                                                                                    Payashi, H., Yoneda, A. and Imamura, T.
Hayashi, H., Yoneda, A. and Imamura, T.
Direct Submission

Direct Submission

Submitted (19-MAR-1999) Toru Imamura, National Institute of
Bioscience and Human Technology, Biosignaling Department; 1-1
Higashi, Tsukuba, Ibaraki 305-8566, Japan

(E-mail:imamura@nibh.go.jp, Tel:81-298-54-6072, Fax:81-298-54-6149)

Location/Qualifiers

1. 2176
/organism="Mus musculus"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (sites)
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                      ABU25198 2176 bp mRNA linear
Mus musculus mRNA for alpha-1,6-fucosyltransferase,
AB025198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mkNA"
/db_xref="taxon:10090"
/sex="male"
/tissue_type="cerebrum"
/dev gagge="adult"
                                                                                    AB025198.1 GI:4586553
alpha-1,6-fucosyltransferase.
Mus musculus (house mouse)
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ilarity 99.8%;
Conservative (
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                                                                                             CTCATCTTGGAATCTCAGAATTGGCGCTATGCTACTGGTGGATGGGAAGACTGTTTAGA
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                                                                           CTCATCTTGGAATCTCAGAATTGGCCCCTATGCTACTGGTGGATGGGAGACTGTGTTTAGA
                                                                                                                                                CCTGTAAGTGAGACATGTACAGACAGATCTGGCCTCTCCACTGGACACTGGTCAGGTGAA
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GYGCQLHHVVYCFMIAYGTQRTLJESQNWRYATGGMETVFRPVSETCTDRSGISTGH
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Homo sapiens
Homo sapiens
Bukaryota; Metazaa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1759)
Taniguchi,N., Seki.T. and Pujiyama,K.
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CCTCCATATTTACCCTTGGCTGTACCAGAAGACCTCGCAGATCGACTGTACGAGTGGAGTGCAT
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Plant cells having function to add animal type sugar chain
Patent: JP 2001333787-A 1 04-DEC-2001;
NAOYUKI TANIGUCHI, TATSUJI SEKI, KAZUHITO FUJIYAMA
OS Homo sapiens (human)
PN JP 2001333787-A/1
PD 04-DEC-2001
PF 06-MAR-2001 JP 2001062704
PI NAOYUKI TANIGUCHI, TATSUJI SEKI, KAZUHITO FUJIYAMA PC
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/organism="Homo sapiens"
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/YFTYPEAEK"
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Purification and cDNA cloning of
GDP-L-Fuc:N-acetyl-beta-D-glucosaminide:alphal-6 fucosyltransferase
(alphal-6 FucT) from human gastric cancer MKN45 cells
J. Biochem. 121 (3), 626-632 (1997)
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                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (18-NOV-1996) Naoyuki Taniguchi, Osaka University Medi
School, Department of Biochemistry; Yamadaoka 2-2, Suita, Osaka
565, Japan (E-mail:proftani@biochem.med.osaka-u.ac.jp,
Tel:81-6-879-3420, Fax.81-6-879-3429)
Location/Qualifiers
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.mRNA for alpha-1,6-fucosyltransferase, complete cds.
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PN JP 1998084975-A/1
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Taniguchi, M., Uozumi, H. and Yanagiya, S.
ALPHA-1, 6-FUCOSYLTRANSFERASE GENE DERIVED FROM HUMAN
Patent: JP 1998084975-A 1 07-APR-1998;
TOYOBO CO LID
OS HOMO sapiens (human)
N JP 1998084975-A/1
PD 07-APR-1997 JP 1997159692
PP 17-UUN-1997 JP 1997159692
PP 22-UUL-1996 JP 96P 192260
                   1403 TACCCCAATTATAGAGATTATTAGTGATAACTCTATTTCCTGGTCAGCTGGACTGCACAAT
                                                                                      GACTTCCTAGTGTGTACTTTTTCATCCCAGGTCTGTCGAGTTGCTTATGAAATTATGCAA
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Human mRNA for alpha-1

E15725

E15725.1 GI:5710408

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Homo sapiens (human)

Homo sapiens
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Homo sapiens mRNA for alpha6-fucosyltransferase (FUT8 gene), clone
                                                                                                                                                                                           TGGCTGGAAAAGGAAATAGAAGAAGCACCAAGAAGCTTGGCTTCAAACATCCAGTTATT
                                                    TGGCTAGAAAAAGAAATAGAAGAAGCCACCAAGAAGCTTGGCTTCAAAAAACATCCAGTTATT
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alpha6-fucosyltransferase are expressed early in

(bases 1 to 2796) human embryogenesis Unpublished Oriol, R. Splice variants of

Oriol, R. Direct Submission

REFERENCE AUTHORS TITLE

JOURNAL TITLE

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

Homo sapiens

REFERENCE AUTHORS

Mollicone, R., Michalski, J.C., Bauvy, C., Cailleau-Thomas, A., Candelier, J.J., Martinez-Duncker, I., Breton, C., Codogno, P. and

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/product="alpha6-fucosyltransferase"
/product="alpha6-fucosyltransferase"
/product="alpha6-fucosyltransferase"
/product="alpha6-fucosyltransferase"
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/db.xref="Gal72820808"
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/translation="MRPWTGSWRWIMLILFAWGTLFYIGGHLVRDNDHPDHSSRELS
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RSIMTDLYYLSGTDGAGDWREKEAMPFLOSELKTYLONPKDCSKAKKLVONINKGC
GYGCOLHHVYYCPWIAYGTORTLLESQNWRYATGWRGYTVFRPVSETCTDRSGISTGH
WSGEVKDKNVQVVELPIVDSLHPRPPYLPLAVPEDBLADRLVRVHGDPAVWWSGFVKY
LIRPOPWLEKEIREAFKKLGFRHPYTGHVRRTDKVGTAAAFHIE EBYMWHVSEHFOL
LARRMQVDKKRVYLATDDFSLLKEAKTYPRYSFISDNSISSAGLHNRYTENGL
LADTHFLSQADFLVCTFSSQVCRVAYEIMQTLHPDASANFHSLDDIYYFGGGNANNQI
AIYAHQPRAADEIPWEFGDIIGVAGNHWDGYSKGVNRKLGRTGLYPSYKVREKIETVK
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| EC_number="2.4.1.68"
| function="adds fucose in alpha1,6 linkage to the internal
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KILAKLERLKQQNEDLRRMAESLRIPEGPIDQGPAIGRVRVLEEQLVKAKEQIENYKK
                                                                                                                                                                                                                                                                               HSY17976 11-SEP-1998 Homo sapiens mRNA for glycoprotein 6-alpha-L-fucosyltransferase,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                              1826 GGCCAGAATGCCCACAAATTGCCATTTATGCTCACCAACCCGGAACTGCAGAA
                                                                                                                                                 1946 AAAGGTGTCAACAGGAAATTGGGAAGGACGGCCTATATCCCTCCTACAAGTTCGAGAG
                                                                                             1886 ATTCCCATGGAACCTGGAGATATCATTGGTGTGCTGGAAATCATTGGGATGGCTATTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Differential splice variants of human FUT8 embryonic cDNA
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Submitted (19-AUG-1998) A.L.V. Cailleau, INSERM U178, 16
Couturier, 94807 Villejuif Cedex, FRANCE
Related entry: D89289.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Cailleau, A., Balanzino, L., Candelier, J.J., Oriol, R. and Mollicone, R.
                                                                                                                                                                                              AAGATAGAAACAGTCAAGTATCCCACATATCCTGAAGCTGAAAATA 1727
                                                                                                                                                                                                                                                                                                                                                     FUT8 gene; glycoprotein 6-alpha-L-fucosyltransferase.
Homo sapiens (human)
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Cailleau, A.L.V.
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WSGCYCKKNYQVYDELEYDSLHRPRPYLDLAVPEDLADRLYKHGDPAVWWYSGPVK
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/ product="alpha6-fucosyltransferase"
/ product="alpha6-fucosyltransferase"
/ protein id="CAD62445.1"
/ db. xref="di:28200810"
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/ gtrkGickChHaVVGTRIAYGTQRTLILESQWRWYATGGWETVFRVGSPTCTDRSGISTGH
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AIYAHQPRTADEIPWEPGDIIGVAGNHWDGYSKGVNRKLGRTGLYPSYKVREKIETVK
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/gene="FUT8"

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/EC_number="2.4.1.68"

/function="adds fucose in alphal,6 linkage to the internal

GloNAc of the core chitobiose"

/codon_start=1
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                           HSA539536 2902 bp mRNA linear PRI 03-FEB-2003
Homo sapiens mRNA for alpha6-fucosyltransferase (FUT8 gene), clone
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (31-JAN-2003) Oriol R., U504, Inserm, 16 Av. Paul
Vaillant-Couturier, 94807, FRANCE
Location/Qualifiers
                                                                                                                                                                                      Mollicone, R., Michalski, J.C., Bauvy, C., Cailleau-Thomas, A., Candelier, J.J., Martinez-Duncker, I., Breton, C., Codogno, P.
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0; Mismatches 141; Indels
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/clone="CD-12"
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/dev grage="40-70 days"
/country="France:Paris"
                                                                                  AJ539536.1 GI:28200809
alpha6-fucosyltransferase; FUT8 gene.
Homo sapiens (human)
Homo sapiens
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/gene="FUT8"
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Oriol, R.
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1406 GGAGTCCATGTCAGACGACAGACAAAGTGGGAACAGAAGCTGCCTTCCATCCCATTGAA 1465
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QTRNGLGKDHEILRRRIENGAKELWFFLQSELKKLKNLEGNELQRHADEFLLDLGHHE
RSIMTDLYYLSQTDGAGDWREKEAKDLTELVQRRITYLQNPKDCSKAKKLVCNINKGC
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product="gl1/coprotein 6-alpha-L-fucosyltransferase"
protein id="CAA76986.1"
db_xref="G1:3451265"
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Pred. No. 0;
0; Mismatches 141;
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   stage="40~70 days"
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/gene="FUT8"
/EC number="2.4.1.68"
/note="allele I"
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2869. .2874
/gene="FUT8"
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/gene="FUT8"
/note="C"
/dev_stage="4
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/gene="PUT8"
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/gene="FUT8"
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/gene="FiJT8"
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/gene="FUT8"
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Matches 1586; Conservative
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Homo sapiens mRNA for glycoprotein 6-alpha-L-fucosyltransferase,
                      1466 GAGTACATGGTGCATGTTGAAGAACATTTTCAGCTTCTTGCACGAGAATGCAAGTGGAC 1525
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (19-AUG-1998) A.L.V. Cailleau, INSERM U178, 16 av P.V.
Couturier, 94007 Villejuif Cedex, FRANCE
Related entry: D89289.
Location/Qualifiers
                                                                                             1526 AAAAAAAGGGGTATTTGGCCACAGATGACCCTTCTTTATTAAAGGAGGCAAAAACAAAG
                                                                                                                                                                 1586 TACCCCAATTATGAATTTATTAGTGATAACTCTATTTCCTGGTCAGCTGGACTGCACAAT
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                                                                          AAAAAAAGAGTATATCTGGCTACTGATGATCCTACTTTGTTAAAGGAGGAAAGACAAAG
                                                                                                                                              TACTCCAATTATGAATTTATTAGTGATAACTCTATTTCTTGGTCAGCTGGACTACAAT
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Homo sapiens (human)
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Cailleau, A., Balanzino, L., Candelier, J.J., Oriol, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="FUT8 transcript Al"
tissue type="whole embryo"
/dev stage="40-70 days"
1. .3186
/gene="FUT8"
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Mammalia; Eutheria; Primates;
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| /gene="FUT8"
| /note="A"
| 390. .488
| /gene="FUT8"
| /note="C"
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/gene="FUT8"
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Cailleau, A.L.V.
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Homo:sapiens mRNA for glycoprotein 6-alpha-L-fucosyltransferase
transcript Al.
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Catarrhini, Hominidae, Homo.
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                                                                       ACCCTGCATCCTGATGCCTCTGCGAACTTCCATTCTTTGGATGACATCTACTATTTTGGA
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Submitted (19-AUG-1998) A.L.V. Cailleau, INSERM U178, 16
Couturier, 94807 Villejuif Cedex, FRANCE
Related entry: D89289.
Location/Qualifiers
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Y17978.1 GI:3451266
FUT8 gene: glycoprotein 6-alpha-L-fucosyltransferase
Homo sapiens (human)
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TLAAKLEKLYQNEDIRRAMSEIRIPEPEPIDGPAIGRYVEKGENEVYKK
OTTAAKLEKLYQNEDIRRAMSEIRIPEPEPIDGSELKKIKNLEGNEIGRHADEFLLDLGHHS
RSIMTDLYYLSQTORRIPENGAKELWFPLGSELKKILKNUEGNEIGRHADEFLLDLGHHS
RSIMTDLYYLSQTORRILESGONWRYATGGWETVRPKOKTAKALVUNINKG
GYGCQLHHVVYCEMIAYGTORTLILESGONWRYATGGWETVRPWGEPTSTGH
WSGEVKDRWVVVELPIVDSLHPRPPYLPLAVPEDLADRLVRPWGGPYVY
LIRPQPWLEKEIEBATKKLGFKGHVIGYHVRRTDKVGTPRAFHPIEBYWWYSGPYVY
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AIYAHOPRTABEIPMEFGDIIGVAGNHWDGYSKGVNRKLGRTGLYPSYKVREKIETVK
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/db_xref="G1:3451267"
/db_xref="SPTREMBL:000235"
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product="glycoprotein
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/gene="FUT8"
note="putative"
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AIYAHQPRTADBIPWEPGDIIGVAGNHWDGYSKGVNRKLGRTGLYPSYKVREKIETVK
                                                                                                                                                        HSY17979 3280 bp mRNA linear PRI 06-NOV-1998
Homo sapiens mRNA for glycoprotein 6-alpha-L-fucosyltransferase
2337 AAAGGTGTCAACAGGAAATTGGGAAGGACGGGCCTATATCCCTCCTACAAAGTTCGAGAG 2396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (19-AUG-1998) A.L.V. Cailleau, INSERM U178, 16 av P.V. Couturier, 94807 Villejuif Cedex, FRANCE Related entry: D89289: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    Mollicone,R.
Differential splice variants of human FUT8 embryonic cDNA
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                                                                    2397 AAGATAGAAACGGTCAAGTACCCCACATATCCTGAGGCTGAGAATA 2443
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FUT8 gene; glycoprotein 6-alpha-L-fucosyltransferase.
Homo sapiens (human)
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tissue_type="whole embryo"
'dev_stage="40-70 days"
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/db_xref="taxon:9606"
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Pred. No. 0;
0; Mismatches 141; Indels
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/gene="FUT8"
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Best Local Similarity 91.8%;
Matches 1586; Conservative
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Oriol, R. Splice variants of alpha6-fucosyltransferase are expressed early in

human embryogenesis Unpublished (bases 1 to 3568)

Oriol, R.

Mollicone, R., Michalski, J.C., Bauvy, C., Cailleau-Thomas, A., Caidelier, J.J., Martinez-Duncker, I., Breton, C., Codogno, P.

Direct Submission
Submitted (06-JAN-2003) Oriol R., U504, INSERM, 16 Avenue Paul
Submitted (06-JAN-2003) Oriol R., U504, INSERM, 16 Avenue Paul
Vaillant-Couturier, Villejuif, 94807, FRANCE
related splice variants AJ536053.1, AJ536054.1 and AJ536056.1.
Location/Qualifiers

1. .3568 /organism="Homo sapiens"

/mol\_type="mRNA" /db\_xref="taxon:9606" /chromoscme="14"

/map="14q23.2"

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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CCTGTAAGTGAGACATGCACAGACAGATCTGGCATCTCCACTGGACACTGGTCAGGTGAA 1556
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                                                                        CCTCCTTACTTACCACTGTTCCAGAAGACCTTGCAGACCGACTCCTAAGAGTCCAT
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FC\_number="2.4.1.68" function="adds fuc in the core chitobiose"

'gene="FUT8"

.098 .2825 gene="FUT8'

codon\_start=1

/clone="£2D-L1" /tissue\_type="whole embryo" /dev\_stage="40-70 days" /country="France:Paris"

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/brotein id="CAD5926.1"
/brotein
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ILDIHPLSQKRVYLATDDPSLLKEAKTYFVPYEISDNSISWSAGLHNRYTENSLRGV
ALYAHQPRADDFLVCTFSSQVCRVAYEIMQTLHPDASANFHSLDDIYYFGGQNAHNQI
AIYAHQPRFADEIPMEPGDIIGVAGSHHWDGYSKGVNRKLGRTGLYPSYKVREKIETVK
YPTYPEAEK"
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0; Mismatches 1
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Matches 1586; Conservative
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Homo sapiens mRNA for alpha6-fucosyltransferase (FUT8 gene), splice
variant B5.
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1217

120

1277

AJ536055
AJ536055.1 GI:275523399
alphae-fucosyltransferase; FUT8 gene.
Homo sapiens (human)
Homo sapiens

VERSION KEYWORDS SOURCE ORGANISM

LOCUS DEFINITION RESULT 15 HSA536055

ACCESSION

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(c) 1993 - 2004 Compugen Ltd.
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Yamano K, Yamasaki M, Hanai N;
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Cells producing antibody compositions including antibody fragments and fusion proteins with Fc domain of antibody, useful for prevention or treatment of cancer, immune diseases, circulatory diseases and infections -

Claim 32; Page 4-11; 314pp; Japanese.

This invention relates to novel method for antibody production comprising a Chinese hemster ovarian tissue-originated (THO) cell transferred with a gene encoding an antibody molecule for producing a composition comprising an antibody molecule with an Fc domain bonded to the Nelyvoside linkage complex sugar chain. The produced antibody compositions are drugs for prevention or treatment of diseases accompanying tumour, allergy or inflammation, autoimmune diseases, circulatory diseases, and viral and bacterial infections. The antibodies can be stably produced using the method of the invention with high binding activity and potency thus leading to high safety and reduced side effects when applied alone or in combination with other drugs for therapy. The present sequence represents a nucleotide molecule used in the method of the invention.

Sequence 1728 BP; 529 A; 365 C; 400 G; 434 T; 0 other;

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ö 120 180 360 420 099 120 180 240 240 300 300 360 420 480 480 540 540 900 900 99 GGTTGTCAACTCCATCACGTGGTCTACTGTTTCATGATTGCTTATGGCACCCAGCGAACA 720 9 9 TTGTTATTTTATATAGGTGGTCATTTGGTTCGAGATAATGACCACCCTGATCACTCCCAGC AGGCGAATGGCTGAGTCTCTCCGAATACCAGAAGGCCCCATTGACCAGGGGACAGCTACA GAAAAAAGGGCCAAAGATCTGACAGAGCTGGTCCAGCGGAGAATAACATATCTCCAGAAT ATGCGGGCATGGACTGGTTCCTGGCGTTGGATTATGCTCATTCTTTTTGCCTGGGGGACC TIGITATITITATATAGGIGGICATITGGTICGAGATAATGACCACCCTGATCACTCCAGC AGAGAACTCTCCAAGATTCTTGCAAAGCTTGAACGCTTAAAAACAGCAAAAATGAAGACTTG agagaacrcrccaagarrcrrgcaaagcrrgaacgcrraaaacagcaaaargaagacrrg AGGCGAATGGCTGAGTCTCTCCGAATACCAGAAGGCCCCATTGACCAGGGGACAGCTACA GGAAGAGTCCGTGTTTTAGAAGAACAGCTTGTTAAGGCCAAAGAACAGATTGAAAATTAC AAGAAACAAGCTAGAAATGGTCTGGGGGAAGGATCATGAAATCTTAAGAAGGAGGATTGAA AAGAAACTAGAAATGCTGGGGAAGGATCATGAAATCTTAAGAAGGAGATTGAA **AATGGAGCTAAAAGAGCTCTGGTTTTTTTTTTACAAAGCGAACTGAAGAAATTAAAAGCATTTA** AATGGAGCTAAAGAGCTCTGGTTTTTTCTACAAAGCGAACTGAAGAAATTAAAGCATTTA GAAGGAAATGAACTCCAAAGACATGCAGATGAAATTCTTTTGGATTAGGACACCATGAA GAAGGAAATGAACTCCAAAGACATGCAGATGAAATTCTTTTGGATTTAGGACACCATGAA **AGGTCTATCATGACAGATCTATACTACCTCAGTCAAACAGATGGAGCAGGGGATTGGCGT** AGGTCTATCATGACAGATCTATACTACCTCAGTCAAACAGATGGAGCAGGGGATTGGCGT GAAAAAGAGGCCAAAGATCTGACAGAGCTGGTCCAGCGGAGAATAACATATCTCCCAGAAT CCTAAGGACTGCAGCAAAGCCAGGAAGCTGGTGTGTAACATCAATAAAGGCTGTGGCTAT Gaps .; 0 24; Length 1728; Indels . 0 DB ; Score 1728; I; Pred. No. 0; 0; Mismatches ATGCGGCCATGGACTGGTTCCTGGCGTTGGATTA Query Match 100.0%; Best Local Similarity 100.0%; Matches 1728; Conservative 0, 61 19 121 121 181 181 241 301 301 361 361 421 421 481 481 541 541 601 199 601

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RESULT

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                                                                                 Antibody production; cytostatic; immunomodulator; vasotropic; virucide; antibactoria!, antiinflammatory; antiallergic; allergy; inflammation; autoimmune disease; Chinese hamster ovarian tissue-originated cell; CHO tumour; circulatory disease; infection; primer; ss.
                                                                                                                                                                                                                                                                                                                     Cells producing antibody compositions including antibody fragments and fusion proteins with Fc domain of antibody, useful for prevention or treatment of cancer, immune diseases, circulatory diseases and
                                                                                                                                                                                                                                                                                                                                                                                                               transferred with a gene encoding an antibody molecule for producing a composition comprising an antibody molecule with an Fc domain bonded to the Neglycoside linkage complex sugar chain. The produced antibody compositions are drugs for prevention or treatment of diseases accompanying tumour, allergy or inflammation, autoimmune diseases, antibodies can be stably produced using the method of the invention with high binding activity and potency thus leading to high safety and reduced side effects when applied alone or in combination with other molecule used in the method of the invention.
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Hanai N;
                                                            Antibody production method related cDNA #1.
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BP.
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Yamasaki M
 2008
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                                        (first entry)
                                                                                                                                                                                                                                             (KYOW ) KYOWA HAKKO KOGYO
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Matches 1638; Conservative
 standard; cDNA;
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                                                                                                                                      Cricetulus griseus
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Hosaka E,
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1360 TACTCCAATTATGAATTTATTAGTGATAACTCTATTCTTGGTCAGCTGGACTACACAC 1419 819 666 300 360 459 420 519 480 579 540 639 900 669 99 759 720 780 879 840 939 900 960 GAAGGAAACGAACTCCAAAGACATGCAGATGAAATTCTTTTGGATTTAGGACATCATGAA GGATGTCAACTCCATCATGTGGTTTACTGCTTCATGATTGCTTATGGCACCCAGCGAACA GTAAATGACAAAACATTCAAGTGGTCGAGCTCCCCATTGTAGACAGCCTCCATCCTCGG 1000 CCTCCTTACTTACCCTTGGCTGTACCAGAAGACCTTGCAGATCGACTCCTGAGAGTCCAT 1120 TGGCTGGAAAGGGAAAYAQAAGAAACCACCAAGAAGCTTGGCTTCAAACATCCAGTTATT GGAGTCCATGTCAGACACACAGACAAAGTGGGAACAGAAGCAGCCTTCCACCCCATCGAG 1180 GGAGTCCATGTCAGACGACTGACAAAGTGGGAACAGAAGAGCAGCCTTCCATCCCATTGAG 340 GGAAGAGTCCGTGTTTYAGAAGAACAGCTTGTTAAGGCCAAAGAACAGATTGAAAATTAC 460 AATGGAGCTAAAGAGC?CTGGTTTTTTCTACAAAGTGAATTGAAGAAATTAAAGAAATTA AGGICTATCATGACAGNICTATACTACCTCAGTCAAACAGATGGAGCAGGGGATTGGCGT 541 GAAAAAGAGGCCAAAGNTCTGACAGAGCTGGTCCAGCGGAGAATAACATATCTCCAGAAT CCTAAGGACTGCAGCAAAGCTGGTGTGTAACATCAATAAAGGCTGTGGCTAT GGTTGTCAACTCCATCACGTGGTCTACTGTTTCATGCTTATGGCACCCAGCGAACA CTCATCTTGGAATCTCNGAATTGGCGCTATGCTACTGGTGGATGGGAGACTGTTTAGA CCTGTAAGTGAGACATYTACAGACAGATCTGGCCTCTCCACTGGACACTCGGTGAA 880 CCTGTAAGTGAGACAT;CACAGACAGGTCTGGCCTCTCCACTGGACACTGGTCAGGTGAA 1060 GGTGATCCTGCAGTGT-GTGGGGTATCCCAGTTTGTCAATACTTGATCCGTCCACAACCT TGGCTGGAAAAGGAAA'TAGAAGAAGCCACCAAGAAGCTTGGCTTCAAACATCCAGTTATT 1201 AAAAAAAGAGTATATCTGGCTACTGATGATCCTACTTTGTTAAAGGAGGCAAAGACAAAG TACTCCAATTATGAATTTAGTGATAACTCTATTTCTTGGTCAGCTGGACTACAAT AATGGAGCTAAAGAGCCCTGGTTTTTTTTTTCTACAAAGCGAACTGAAGAAATTAAAGCATTTA GAAGGAAATGAACTCCNAAGACATGCAGATGAAATTCTTTTGGATTTAGGACACCCATGAA CCTCCTTACTTACCAC'IGGCTGTTCCAGAAGACCTTGCAGACCGACTCCTAAGAGTCCAT GGTGACCCTGCAGTGT:GTGGGTGTCCCAGTTTGTCAAATACTTGATTCGTCCACAACCT

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CICATCITGGAAICICAGAAIIGGCGCTAIGCIACIGGIGGAIGGGAGACIGIGITIAGA 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AATGGAGCTAAAAGAGCTCTGGTTTTTTCTACAAAGCGAACTGAAGAAATTAAAAGCATTTA
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                                                                                       Score 1501.4; DB 24; Lengt
Pred. No. 0;
0; Mismatches 141; Indels
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Best Local Similarity 91.8%;
Matches 1586; Conservative (
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                                                                                                                                                                    GGCCAAAATGCCCACAAACCAGATTGCAGTTTATCCTCACCAACCTGGAACTAAAGAGGAAA
                                                                                                                                                                                                                        ATCCCCATGGAACCTGGAGATATCATTGGTGTGGCTGGAAACCATTGGAATGGTTACTCT
       CGGTACACAGAAAATTCACTTCGGGGTGTGATCCTGGATATACACTTTCTCTCACAGGCT
                    GACTTTCTAGTGTACTTTTCATCCCAGGTCTGTCGGGGTTGCTTATGAAATCATGCAA
                                                                   ACCCTGCATCCTGATGCCTCTGCGAACTTCCATTCTTTGGATGACATCTACTATTTTGGA
                                                                                                                  GGCCAAAATGCCCACAATCAGATTGCTGTTTATCCTCACAAACCTCGAACTGAAGAGGAA
                                                                                                                                                                                                     ATTCCAATGGAACCTGGAGATATCATTGGTGGCTGGAAACCATTGGGATGGTTATTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycoprotein; alphal, 6-fucosyl transferase; alphal, 6-FT;
                                                                                                                                                                                                                                                                                                                 A plant cell with an animal type sugar chain adding function, preparation of a glycoprotein with an animal type sugar chain
                                                                                                                                                                                                                                                                                                    AAGATAGAAACAGTCAAGTATCCCACATATCCTGAAGCTGAAAAATAG 1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17..1744
/*tag= a
/product= "Alphal,6-fucosyl transferase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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(SEKI/) SEKI T.
(FUJI/) FUJIYAMA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
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P-PSDB; ABB08405.
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AAT76573 and AAT76574 represent the coding sequences for the pig and human alpha 1-6 fucosyltransferases of the invention, respectively. The encoded enzyme transfers fucose from guanosine diphosphate to the 6-hydroxyl group of the GloNac nearest to R in the receptor molecule: GlcNacbeta 1-Manalpha 1-5) Manbeta 1-4GlCNAccheta 1-ZManalpha 1-5) Manbeta 1-4GlCNAccheta 1-ZManalpha 1-6) GlcNacbeta 1-2Manalpha 1-6) GlcNacbeta 1-4(Fucalpha 1-6) GlcNacbeta 1-2Manalpha 1-6) GlcNacbeta 1-6 GlcNacbeta 1-2Manalpha 1-6) GlcNacbeta 1-6 G
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synthesis and modification of sugar chains and used as an antigen
for production of diagnowitc antibodies
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24-JUN-1996;
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Matches 1586;
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CCTCCATATTTACCCTTGGCTGTACCAGAAGACCTCGCAGATCGACTTGTACGAGTGCAT
                                                  GGTGACCCTGCAGTGTGGGTGTCCCAGTTTGTCAATACTTGATTCGTCCACAACCT
                                                                                                    GGTGACCCTGCAGTGTGGTGTCTCAGTTTGTCAAATACTTGATCCGCCCACAGCCT
                                                                                                                                                         TGGCTGGAAAAGGAAATAGAAGGAAGCCACCAAGAAGCTTGGCTTCAAACATCCAGTTATT
                                                                                                                                                                                                                                                                   GGAGTCCATGTCAGACGCACAGACAAGTGGGAACAGAAGCAGCCTTCCACCCCATCGAG
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) assessing the prostate cell carcinogenic potential of a compound;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
ACACTACATCCTGATGCCTCTGCAAACTTCCATTCTTAGATGACATCTACTATTTTGGG
                                                            ATTCCAATGGAACCTGGAGATATCATTGGTGTGGCTGGAAACCATTGGGATGGTTATTCT
                                                                                                                                             ATTCCCATGGAACCTGGAGATATCATTGGTGTGGCTGGAAATCATTGGGATGGCTATTCT
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09-JUN-2000; 2
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13-DEC-2000; 2
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86.9%; Score 1501.4;

Best Local Similarity 91.8%; Pred. No. 0;

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(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
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                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, usef for detecting presence of prostate cancer
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                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid molecule (I) common a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
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Pred. No. 0;
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                                                                                                                             PREDICTIVE
17-FEB-2000, 2000US-183319P.
16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
09-UJN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
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Local Similarity 91.8%;
Hes 1586; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 4277~\mathrm{human} colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
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                                                                                                                                                                                                                                                                  Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; chromosome 14; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.2%; Score 1490; DB 22; Length 3007; 91.7%; Pred. No. 0; ive 1; Mismatches 141; Indels 1;
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N.B. Pages 666 to 6
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human alpha 1-6 fucosyltransferases of the invention, respectively. The concoded enzyme transferases of the invention, respectively. The encoded enzyme transfers fucose from ganosine diphosphate to the concoded enzyme transfers fucose from ganosine diphosphate to the concoded enzyme transfers fucose from ganosine diphosphate to the concoded enzyme transfers fucose from ganosine diphosphate to the concoded enzyme the GICNAcher at 1-2 manalpha 1-3) Manbeta 1-4 dicNAcher at 0 give (GICNAchera 1-3) Manbeta 1-4 dicNAchera 1-4 (Fucalpha 1-3) Manbeta 1-3) Manbeta 1-3 manbeta 1-4 dicNAchera 1-4 (Fucalpha 1-6) GICNAcher. It has an optimum pH of about 7.0 (pig) or 7.5 (human), and is stable over the copymenture of the enzyme is 30-37 degrees C. A bivalent metal is not required for activity of the enzyme, and the enzyme is not inhibited in complete the presence of 5 mM EDTA. The enzyme is useful in the synthesis and modification of sugar chains, and as antigen for the production of antibodies recognishing the enzyme. The antibodies can be used for the concoded enzyme. The antibodies can be used for the concoded enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunologically functional molecule, immune system; immunomodulation; glycosylation; fucose; N-acetylglucosamine; cancer; circulatory disease; viral infection; bacterial infection; allergy; autoimmune disease; inflammation; antibody; rat; FUT8; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for controlling the activity of an immunologically functional molecule (e.g., an antibody) where the control is effected by the presence or absence of fucose bound to an N-acetylglucosamine residue at the reducing end of the sugar chain on the immunologically functional molecule. The invention also relates to methods for the diagnosis, prevention or treatment of diseases which involve the modified immunologically functional molecule, and agents which stimulate the activity of an immunologically functional molecule. The methods of the invention are used for the diagnosis, treatment and prevention of a broad range of diseases including cancer, circulatory disease, viral or bacterial infection, allergy, autoimmune disease and inflammation. The present sequence represents a rat FUT8 cDNA isolated in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Control of activity of antibodies and other immunologically functional molecules by addition or removal of fucose from sugar chain for diagnosis and treatment of cancer, allergy and other diseases
                                  1621 AAAGGTGTTAACAGAAAACTGGGAAGGACGGGCCTATATCCCTCCTACAAAGTTCGAGAG
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Pred. No. 1.4e-272;
0; Mismatches 30;
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Anazawa H;
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Best Local Similarity 96.3%;
Matches 949; Conservative 0
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S, Kanda Y,
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Antibody production; cytostatic; immunomodulator; vasotropic; virucide; antibacterial; antiinflammatory; antiallergic; allergy; inflammation; autoimmune disease; Chinese hamater ovarian tissue-originated cell; CHO; tumour; circulatory disease; infection; primer; 88.

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                                           AGTGAATGACAAAAATATTCAAGTGGTGGAGCTCCCCCATTGTAGAGACAGCCTTCATCCTCG
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Cells producing antibody compositions including antibody fragments ar fusion proteins with Fc domain of antibody, useful for prevention or treatment of cancer, immune diseases, circulatory diseases and

Example 9; Page 13-14; 314pp; Japanese

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Uchida K, Hanai N;

Nakamura K, Uc Yamasaki M,

Satoh M, N Yamano K,

Kanda Y, S Hosaka E,

WPI; 2002-340182/37.

(KYOW ) KYOWA HAKKO KOGYO KK 06-OCT-2000; 2000JP-0308526. 05-OCT-2001; 2001WO-JP08804

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                 TAAAAAAAGAGTATATCTGGCTACTGATGATCCTACTTTGTTAAAGGAGGAGGCAAAGACAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for controlling the activity of an immunologically functional molecule (e.g., an antibody) where the control is effected by the presence or absence of fucose bound to an N-acetylglucosamine residue at the reducing end of the sugar chain on the immunologically functional molecule. The invention also relates to methods for the diagnosis, prevention or treatment of diseases which involve the modified immunologically functional molecule, and agents which stimulate the activity of an immunologically functional molecule. The methods of the invention are used for the diagnosis, treatment and prevention of a broad range of diseases including cancer, circulatory disease, viral or bacterial infection, allergy, autoimmune disease and inflammation. The present sequence represents a Chinese hamster FUTB CDNA isolated in an exemplification of the invention.
                                                                                                                                                                                     Control of activity of antibodies and other immunologically functional molecules by addition or removal of fucose from sugar chain for diagnosis and treatment of cancer, allergy and other diseases
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Pred. No. 2.2e-261;
0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                     Example 8; Page 72-73; 81pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                      Antibody production; cytostatic; immunomodulator; vasotropic; virucide; antibacterial; antiinflammatory; antiallargic; allergy; inflammation; autoimmune disease; Chinese hamster ovarian tissue-originated cell; CHO; tumour; circulatory disease; infection; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cells producing antibody compositions including antibody fragments and fusion proteins with Fc domain of antibody, useful for prevention or treatment of cancer, immune diseases, circulatory diseases and
                                                                                                                                                                         This invention relates to novel method for antibody production comprising a Chinese hamster ovarian tissue-originated (GHO) cell transferred with a gene encoding an antibody molecule for producing a composition comprising an antibody molecule with an Fc domain bonded to the N-glycoside linkage complex sugar chain. The produced antibody compositions are drugs for prevention or treatment of diseases accompanying tumour, allergy or inflammation, autoimmune diseases, circulatory diseases, and viral and bacterial infections. The
                      TGACTTCCTTGTGTGTATTTTTTCATCCCAGGTCTGTAGGGTTGCTTATGAAATCATGCA
                                                                   721 AACACTGCATCCTGATGCCTCTGCAAACTTCCATTCTTTAGATGACATCTACTATTTTGG
                                                                                          AGGCCAAAATGCCCACAATCAGATTGCTGTTTATCCTCACAAACCTGAAGTGAAGAGA
                                                                                                       781 AGGCCAAAATGCCCACAACCAGATTGCAGTTTATCCTCACCAACCTGGAACTAAAGAGGA
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                                                                                                                                                                                                                                                                                                                                                  Antibody production method related cDNA
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Yamasaki M,
                                                                                                                                                                                                                   GAAGATAGAAACAGTCAAG 1698
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                                                                                                                                                                                                                                                                                        ABK70036 standard; cDNA;
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Hosaka E, Yamano K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 TAAAAAAGAGTGTATCTGGCCACTGATGACCCTTCTTTGTTAAAGGAGGCAAAGACAAA
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antibodies can be stably produced using the method of the invention with high binding activity and potency thus leading to high safety an reduced side effects when applied alone or in combination with other darugs for therapy. The present sequence represents a nucleotide molecule used in the method of the invention.
                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                           979;
                                                                                                                                                                         DB 24; Length
                                                                                                                                                                                                                                                              720 ACTCATCTTGGAATCTCAGAATTGGCGCTATGCTACTGGTGGATGGG
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                                                                                                                                Sequence 979 BP; 286 A; 227 C; 218 G; 248 T; 0 other;
                                                                                                                                                                       Score 894.2; DB 24;
Pred. No. 2.2e-261;
0; Mismatches 53;
                                                                                                                                                                     Query Match 51.7%;
Best Local Similarity 94.6%;
Matches 926; Conservative 0
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CGTCCACAACCTTGGCTGGAAAAGGAAATAGAAGGAAGCCACCAAGAAGCTTGGCTTCAAA 1068
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                                                                                                           CTAAGAGTCCATGGTCCTGCAGTGTGGTGGTGTCCCCAGTTTGTCAAATACTTGATT
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                                                                       crrcarccccarccrcararrracccrraccraracaaaaaccrcacaaarccacrr
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                                                                                                                                                                                                                                                                                                                 421 CATCCCATTGAAGAGTACATGGTGCATGTTGAAGAACATTTTCAGCTTCTTGCACGCAGA
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alpha 1-6 fucose transferase; anti-human alpha 1-6 fucT; immunoassay;
ds.
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61 ACTGTATTTAGGCCTGTAAGTGAGACATGCACAGACAGATCTGGCATCTCCACTGGACAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an anti-human alpha 1-6 fucose fucosyltransferase (alpha 1-6 fucT, also called alpha 1-6 fucose transferase) antibody. Also described are: (1) a hybridoma producing the above monoclonal antibody; (2) an immunoassay for detecting human alpha 1-6 fucT by using the above antibody or its antibody fragment; and (3) a reagent used for the above immunoassay. The anti-human alpha 1-6 fucT antibody can be used for immunoassay. The present sequence encodes the human alpha 1-6 fucT protein of residues 237 to 575, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                              Human; alpha 1-6 fucosyltransferase; alpha 1-6 fucT; antibody;
alpha 1-6 fucose transferase; anti-human alpha 1-6 fucT; immunoassay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 709 ACCCAGCGAACACTCATCTTGGAATCTCAGAATTGGCGCTATGCTACTGGTGGATGGGAG
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                                                                                                                                                                                                                                                 Human alpha 1-6 fucosyltransferase 237-575 encoding DNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "alpha 1-6 fucosyltransferase 237-575"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel anti-human alphal-6 fucose transferase antibody useful for
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Pred. No. 6.8e-256;
0; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 6-7; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                              1680 GAAGATAGAAACAGTCAAG 1698
                                                              BP.
                                                                                                                                                       AAF87952 standard; DNA; 1017
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Best Local Similarity
Matches 929; Conserv
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421 CATCCTGATGCCTCTGCAACTTCCATTCTTTAGATGACATCTACTATTTTGGGGGCCAG 480
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Matches 711, Conservative
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                                                                                                                                                                                                                                                                                             26-MAR-2002
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ABL04601
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                                                                                                                                                                                                                                                                                                                 The present invention describes an anti-human alpha 1-6 fucose fucosyltransferase (alpha 1-6 fuct, also called alpha 1-6 fucose transferase) antibody. Also described are: (1) a hybridoma producing the above monoclonal antibody; (2) an immunoassay for detecting human alpha 1-6 fucT by using the above antibody or its antibody fragment; and (3) a reagent used for the above immunoassay. The anti-human alpha 1-6 fucT antibody can be used for immunoassay. The present sequence encodes the human alpha 1-6 fucT protein of residues 343 to 575, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1087 CATGTCAGACGCACAGACAAAGTGGGAACAGAAGCAGCCTTCCACCCCATCGAGGAGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAGTATATCTGGCTACTGATGATCCTACTTTGTTAAAGGAGGCAAAGACAAAGTACTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u> AGAGTGTATTTGGCCACAGATGACCCTTCTTTATTAAAGGAGGCAAAAAACAAAGTACCCC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATTATGAATTTATTAGTGATAACTCTATTTTCTTGGTCAGCTGGACTACACAATCGGTAC
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                                                                                   fucosyltransferase 343-575'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 35.0%; Score 604.6; DB 22
Best Local Similarity 91.6%; Pred. No. 2.9e-173;
Matches 640; Conservative 0; Mismatches 59;
                                                                                   /product= "alpha 1-6
                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                              Example 1; Page 7-8; 11pp; Japanese.
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                                                                                                          JP2001011097-A
                sapiens
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                                                                                                                                 16-JAN-2001
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AATGCCCACAATCAGATTGCTGTTTATCCTCACAAACCTCGAACTGAAGAGGAAATTCCA 1566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                               601 Grcalcaggaatroggaaggacggcctatatccctcctaaagtroggagagata
                                                                                                                              ATGGAACCTGGAGATATCATTGGTGTGGCTGGAAACCATTGGGATGGTTATTCTAAAGGT
                                                                                                                                                           1627 ATCAACAGAAAACTTGGAAAAACAGGCTTATATCCCTCCTACAAAGTCCGAGAAGATA
                                                             481 AATGCCCACAATCAAATTGCCATTTATGCTCACCAACCCGAACTGCAGATGAAATTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developmental biology; cell signalling; insecticide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster expressed polynucleotide SEQ ID NO 8285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23; Length 2761;
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                                                                                                                                                                                                                                                                                                                                                                          1687 GAAACAGTCAAGTATCCCACATATCCTGAAGCTGAAAAA 1725
                                                                                                                                                                                                                                                                                                                                                                                                                       GAAACGGTCAAGTACCCCACATATCCTGAGGCTGAGAAA 699
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Pred. No. 3.9e-104;
0; Mismatches 522;
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57.2%;
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical; gene; ss.
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533	ATTGGCGTGAAAAAGGGCCAAAGATCTGACAGAGGTGGTCCAGCGGAGAATAACATATC 592 
593	TCCAGAATCCTAAGGACTGCAGGAAGCCAGGAAGCTGGTGTGTAACATCAATAAAGGGT 652 
653	GIGGCTATGGTTGTCAACTCCATCAGGGGTCTACTGTTTCATGATTGCTTATGGCACCC 712 
713	AGCGAACACTCATCTTGGAATCTCAGAATTGGCGCTATGCTACTGGTGGATGGGAGACTG 772 
173	TGTTTAGACCTGTAAGTGAGACATGTACAGATCTGGCCTCTCCACTGGACACTGGT 832
833	CAGGIGAAGTAAATGACAAAAGATTCAAGIGGICGAGCTCCCCATIGTAGACAGCCTCC 892 
893	ATCCTCGGCCTCCTTACTTACCACTGGCTGTTCCAGAGACCTTGCAGACCGACTCCTAA 952
953 1554 <sup>°</sup>	GAGTCCATGGTGACCCTGCAGTGTGGTGTCCCAGTTTGTCAATACTTGATTCGTC 1012
1013	CACAACCTTGGCTGGAAAAGGAAATAGAAGAGCCACCAAGAAGCTTGGCTTCAAACATC 1072 
1073	CAGTITATIGGAGTCCATGTCAGACGCACAGACGGGAACAGAAGCAGCCTTCCACC 1132
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1193	aagtegataaaaaagagtatatctggctactgatgatcctactttgttaaagaggcaa 1252 
1253	AGACAAAGTACTCCAATTATGAATTTATTAGTGATAACTCTATTTCTTGGTCAGCTGGAC 1312 
1313	TACACAATCGGTACACAGAAAATTCACTTCGGGGTGTGATCCTGGATATACACTTTCTCT 1372 
1373	CACAGGCTGACTTTCTAGTGTACTTTTTCATCCCAGGTCTGTCGGGTTGCTTATGAAA 1432 
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February 2, 2004, 12:05:46; Search time 104.069 Seconds (without alignments) 7328.922 Million cell updates/sec
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GenCore version 5.1.6
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                                                                                                                                                                                                                                                                                                                                                                                                          569978 seqs, 220691566 residues
                                                                                              OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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1728
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents NA:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

						SUMMARIES		
Result	17		Ouerv					
2	No.	Score	Match	Match Length	DB	ID	Description	
•	1	1496.6	86.6	2100	<u> </u> m	US-08-913-805A-9	Sequence 9, Appli	
	8	1496.6	96.6	2100	m	US-09-442-629-9	6	
	٣	1469.4	85.0	1728	m	US-08-913-805A-1	٦,	
	4	1469.4	85.0	1728	٣	US-09-442-629-1	H	
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	9	38.2	2.2	921	4	US-09-328-352-2691	269	
υ	7	38	2.2	1230025	4	US-09-198-452A-1	Sequence 1, Appli	
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	9	37.2	2.2	1596	4	US-09-134-001C-2083	Sequence 2083, Ap	
O	10	36.8	2.1	1750	~	US-08-933-750C-54	Sequence 54, Appl	
O	Ħ	36.8	2.1	1750	٣	US-09-234-613-54	Sequence 54, Appl	
O	12	36	2.1	4517	m	US-09-140-804-9	6	
O	13	36	2.1	4517	4	US-09-686-838B-9	Sequence 9, Appli	
U	14	36	2.1	4517	4	US-09-776-976-5	'n	
υ	15	36	2.1	4517	4	US-09-909-547-5	'n	
	16	35.8	2.1	1664976	4	US-08-916-421B-1	1,	
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U	20	34.2	2.0	602	4	US-09-538-709-21	71,	
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	22	34	2.0	1591	7	US-08-646-981-14	14,	
υ	23	34	2.0	2915	4	US-09-336-115C-5	5, A	
	24	33.8	2.0	805	m	US-08-961-083-139	13	
	25	33.8	2.0	805	4	US-09-536-784-139	Sequence 139, App	
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O	27	33.8	2.0	1041	4	US-09-252-991A-12831	Segmence 12831, A	

13111, A 148, App 1, Appli	4, Appli 2485, Ap	70, Appl 6, Appli	73, Appl	73,	7, Appli	7, Appli	7, Appli	3, Appli	2, Appli	<ol> <li>Appli</li> </ol>	3, Appli	3, Appli	1, Appli
Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-09-252-991A-13111 US-08-961-527-148 US-08-143-219-1	US-09-379-523-4 US-09-134-001C-2485	US-09-397-787-70 US-09-592-998C-6	US-08-887-534A-73	US-09-527-431-73	US-08-699-103B-7	US-09-229-059-7	US-09-628-133-7	US-09-336-115C-3	US-08-973-462-2	US-08-973-462-1	US-09-738-894A-3	US-09-964-469-3	US-09-426-290-1
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28 30	31	33	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

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COMPUTER READBLE FORM:
MEDIUM TYPE: 3 + Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS(MS-DOS 6.2
SOFTWARE: WordPerfect 5.1 Windows
CURRENT APPLICATION DATA:
APPLICATION DATE:
APPLICATION NUMBER: US/08/913,805A
FILING DATE: 7 JAN 1993
CLASSIFCATION A35
PRIOR APPLICATION NUMBER: PCI/JP97/00171
APPLICATION NUMBER: PCI/JP97/00171
APPLICATION NUMBER: JP 192260
FILING DATE: 23 JAN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 10365
APPLICATION NUMBER: JP 10365
APPLICATION NUMBER: JP 10365
APPLICATION NUMBER: JF 101365
APPLICATION NUMBER: JF 101365
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                                                        ; Sequence 9, Application US/08913805A; Patent No. 6054304
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REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2100 base pairs
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STRANDEDNESS: double
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GGTGACCCTGCAGTGTGGTGTCTCAGTTTGTCAAATACTTGATCGGCCCACAGGCT
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SHIBM, Tetsuo
YANAGIDANI, Shusaku
TITLE OF INVENTION: Alpha 1-6 Fucosyltransferase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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STREET: 1025 Connecticut Avenue,
CITY: Washington
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3+ Floppy disk
COMPUTER: IBM PC compatible
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Patent No. 6291219
GENERAL INFORMATION:
APPLICANT: TANIGUCHI, Naoyuki
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                                             Query Match 86.6%; Score 1496.6; Best Local Similarity 91.7%; Pred. No. 0; Matches 1583; Conservative 0; Mismatches
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                                             APPLICATION NUMBER: US/09/442,629
FILING DATE: 18-NO. 6291219-1999
IOR APPLICATION DATA:
FILING DATE: 7 JAN 1998
APPLICATION NUMBER: US/08/913,805A
FILING DATE: 7 JAN 1997
APPLICATION NUMBER: PCT/JD97/00171
FILING DATE: 23 JAN 1997
APPLICATION NUMBER: JP 19260
FILING DATE: 22 JUL 1996
APPLICATION NUMBER: JP 162813
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 16488
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 21 JUN 1996
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1496.6;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                  TWARE: WordPerfect 6.1 Windows APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             NAME: Toffenetti, Judith L.
REGIETRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 2356/3
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NO: 9:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 10365
FILING DATE: 24 JAN 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID
US-09-442-629-9
                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 202-429-1776
TELEFAX: 202-429-0796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2100 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
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91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 91.7
Matches 1583; Conservative
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Pred. No. 0;
0; Mismatches 161;
                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: TANIGUCHI, Nacyuki
APPLICANT: UOZUMI, Nachumi
APPLICANT: SHIBA, TELSUO
APPLICANT: SHIBA, TELSUO
APPLICANT: YANAGIDANI, Shusaku
TITLE OF INVENTION: Alpha 1-6 Fucosyltransferase
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                      STATE: DC
COUNTRY: US
ZIP: 2008
ZIP: 2008
ZIP: 2008
ZIP: 2008
ZIP: 2008
ZIP: 2008
COMPUTER READABLE FORM:
MEDIUM TYPE: 3+ Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WordPerfect 6.1 Windows
CURSINGTON UNMBER: US/08/913,805A
FILING DATE: 7 JAN 1998
CLLASSIFICATION DATA:
APPLICATION NUMBER: PCT/JP97/00171
FILING DATE: 23 JAN 1997
APPLICATION NUMBER: JP 192260
FILING DATE: 23 JAN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 10162813
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 2356/3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 202-429-1776
                                                                                                                                                                             Sequence 1, Application US/08913805A
Patent No. 6054304
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ilarity 90.7%;
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STRANDEDNESS: double
TOPOLOGY: linear
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Matches 1566; Conserv
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US-08-913-805A-1
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                                                                    85.0%; Score 1469.4;
90.7%; Pred. No. 0;
iive 0; Mismatches
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECTLE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
               APPLICATION NUMBER: JP 161648
FILLING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 10365
FILLING DATE: 24 JAN 1996
24 JUN 1996
                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 90.7
Matches 1566; Conservative
FILING DATE:
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US-09-442-629-1
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                                   AAAAAAAGAGTATATCTGGCTACTGATGATCCTACTTTTGTTAAAGGAGGCAAAGGACAAAG
                                                                 AAAAAAGGGTGTATTTGGCCACAGATGACCCTGCTTTGTTAAAAGAGGCAAAAACAAAG
                                                                                                  TACTCCAATTATGAATTTATTAGTGATAACTCTATTTCTTGGTCAGCTGGACTACAAT
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Patent No. 6291219
GENERAL INFORMATION:
APPLICANT: TANIGUCHI, Naoyuki
UOZUMI, Naofumi
SHIBA, Tetsuo
YANAGIDANI, Shusaku
TITLE OF INVENTION: Alpha 1-6 Fucosyltransferase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPARE: WordPerfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/442,629
FILING DATE: 18-No. 6291219-1999
PRIOR APPLICATION NUMBER: US/08/913,805A
FILING DATE: 7 JAN 1998
APPLICATION NUMBER: PCT/UP97/00171
FILING DATE: 23 JAN 1997
APPLICATION NUMBER: PCT/UP97/00171
FILING DATE: 23 JAN 1997
APPLICATION NUMBER: 1992260
FILING DATE: 22 JUL 1996
APPLICATION NUMBER: JP 162813
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COMPUTER READABLE FORM:
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; GENERAL INFORMATION:
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                 CTCATCTTGGAATCTCAGAATTGGCGCTATGCTACTGGTGGATGGGAGACTGTGTTTAGA
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RESULT 5 US-08-232-463-14/c ; Sequence 14, Application US/08232463

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467 TAGGACACCATGAAAGGTCTATCATGACAGATCTATACTACCTCAGTCAAACAGATGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287 AGATTGAAAATTACAAGAAACAAGCTAGAAATGGTCTGGGGAAGGATCATGAAATCTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 GAAGGAGGATTGAAAATGGAGCTAAAAGGCCTCTGGTTTTTTCTACAAAGCGAACTGAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 AGGGGACAGCTACAGGAAGAGTCCGTGTTTTAGAAGAACAGCTTGTTAAGGCCCAAAGAAC
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                                                                                                                                                                                                        ZIP: 22313-0299
ZIP: 22313-0299
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26; Conservative 233; Mismatches 153;
                                                              FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.3%; Score 74; DB 1;
5.3%; Pred. No. 7.4e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                        ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite
CITY: Alexandria
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: PALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.3%;
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IMMEDIATE SOURCE:
CLONE: pTZgpt-Fls
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Best Local Similarity
Matches 26; Conserv
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US-08-232-463-14
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NAME/KEY: misc feature
LOCATION: (420001)..(435060)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (195001)..(210000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc_feature
LOCATION: (210001)..(225000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (180001)..(195000)
OTHER INFORMATION: n=a or c or g or
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INFORMATION: n=a or c or g or
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LOCATION: (135001)..(150000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (150001)..(165000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (105001)..(120000)
OTHER INFORMATION: n=a or c or g
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INFORMATION: n=a or c or g
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LOCATION: (240001)..(255000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (300001)..(315000)
THER INFORMATION: n=a or c or g
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/KEY: misc feature

FION: (330001)...(345000)

RINFORMATION: n=a or c or g
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THER INFORMATION: n=a or c or g

NAME/KEY: misc_feature
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LOCATION: (120001)..(135000)
OTHER INFORMATION: n=a or c or g
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INFORMATION: n=a or c or g
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LOCATION: (165001)..(180000)
OTHER INFORMATION: n=a or c or
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CCCATION: (255001)..(270000)
THER INFORMATION: n=a or c or
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INFORMATION: n=a or c or
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COCATION: (285001)..(300000)
THER INFORMATION: n=a or c or
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LCCATION: (345001)...(360000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc_feature
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OTHER INFORMATION: n=a or c or
NAME/KEY: misc_feature
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...mTON: (225001)..(240000)
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OCATION: (315001)..(330000)
                                                              NAME/KEY: misc feature
LOCATION: (90001)..(105000)
OTHER INFORMATION: n=a or c
          LOCATION: (75001)..(90000)
OTHER INFORMATION: n=a or c
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US-09-198-452A-1/c
Sequence 1, Application US/09198452A
Sequence 1, Application US/09198452A
Sequence 1, Application US/09198452A
GENERAL INPORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1
LENGTH: 1230025
                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 2691
LENGTH: 921
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                            1070 RERRATCGCAAGCTCCCTCGACCTGCAAGCTCGGAATTAATTCTGTGA 1019
587 CATATCTCCAGAATCCTAAGGACTGCAGCAAAGCCAGGAAGCTGGTGTGTAA 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           398 AACTGAAGAAATTAAAGCATTTAGAAGGAAATGAACTCCAAAGACATGCAG 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       665 caaaactrctrtraaargactracaagccartaaaaargcagcactrgcrg 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38.2; DB 4; DC.5.
Pred. No. 0.067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.2%; Score 38.2; Dl
Best Local Similarity 51.5%; Pred. No. 0.06'
Matches 88; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (15001)...(30000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (30001)..(45000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (45001)..(60000)
                                                                                                                                                                  Sequence 2691, Application US/09328352 Patent No. 6562958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-2691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Chlamydia pneumoniae
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OTHER INFORMATION: n=a or c
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LOCATION: (60001)..(75000)
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US-09-328-352-2691
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NAME/KEY: misc_feature
LOCATION: (49501)..(510000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (510001)..(525000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (525001)..(540000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (54001)..(555000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (55501)..(570000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
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LOCATION: (58501)..(600000)

JHER INFORMATION: n=a or c or g or l
NAME/KEY: misc feature

NAME/KEY: misc feature

COCATION: (600001)..(615000)

JHER INFORMATION: n=a or c or g or l
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OTHER INFORMATION: n=a or c or g or NAME/KEY: misc_feature
LOCATION: (720001)..(735000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc feature
LOCATION: (435001)..(450000)
OTHER INFORMATION: n=a or c or g or
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OTHER INFORMATION: n=a or c or g or NAME/KEY: misc_feature
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LOCATION: (615001)..(630000)
JTHER INFORMATION: n=a or c or g or
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OTHER INFORMATION: n=a or c or g or
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LOCATION: (660001)..(675000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc_feature
LOCATION: (675001)..(690000)
LOCATION: (67501)..(690000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc_feature
LOCATION: (69001)..(705000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc_feature
LOCATION: (69001)..(705000)
                                                                           NAME/KEY: misc feature
LOCATION: (450001)..(465000)
OTHER INFORMATION: n=a or c or g or
LOCATION: (465001)..(480000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc feature
LOCATION: (465001)..(480000)
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NAME/KEY: misc feature
OTHER INFORMATION: (490001)..(495000)
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OTHER INFORMATION: n=a or c or g
NAME/KEY: misc feature
OCATION: (75001)..(765000)
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LOCATION: (64501)..(66000)
OTHER INFORMATION: n=a or c or g
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THER INFORMATION: n=a or c or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (630001)..(645000)
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369111 AAArcachaaaracchaaarraacsaccratrarracaacraaaraaaraccarccrcrc 369052 369171 TCCATGTAGTCAAAATAGCTACAAGATTTTTATTCATTATACTCCTCTTGTAAATAAGG 369112 GENERAL INFORMATION:
APPLICANT: Motoharu SEIKI et al.
TITLE OF INVENTION: NOVEL PROTEIN AND MONOCLONAL ANTIBODY SPECIFIC THERETO
TITLE OF INVENTION: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P. 1190 TGCAAGTGGATAAAAAAGAGTATATCTGGCTACTGATGATCCTACTTTGTTAAAGGAGG 1250 CAAAGACAAAGTACTCCAATTATAATTATTAGTGATAACTCTATTTCTTGGTCAGCTG ö 2.2%; Score 38; DB 4; Length 1230025; S6.3%; Pred. No. 9.8; tive 0; Mismatches 55; Indels 0; STREET: 2033 K Street, N.W., Suite 800 CITY: Washington STATE: D.C. E: Diskette, 3.5 inch, 1.44 mb SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,041A APPLICATION NUMBER: PCT/JP96/01956 NAME/KEY: misc\_feature LOCATION: (900001)..(915000) OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc\_feature OTHER INFORMATION: n=a or c or g or NAME/KEY: misc\_feature LCCATION: (82500). (840000) OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature LOCATION: (855001)..(870000) OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature LOCATION: (885001)..(900000) OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature LOCATION: (84001)..(855000) OTHER INFORMATION: n=a or c or g or ; Sequence I, Application US/09000041A ; Patent No. 6191255 January 13, 1998 NAME/KEY: misc feature LOCATION: (87001)..(885000) OTHER INFORMATION: n=a or c or g COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS FILING DATE: July 12, 15 ATTORNEY/AGENT INFORMATION: REFERENCE/DOCKET NUMBER: Query Match
Best Local Similarity 56.3The 71; Conservative NAME: Lee Cheng REGISTRATION NUMBER: COMPUTER READABLE FORM: MEDIUM TYPE: Diskett FILING DATE: January CLASSIFICATION: 536 PRIOR APPLICATION DATA: 369051 CÁTTÁC 369046 : misc feature : (810001)..(8 1310 GACTAC 1315 U.S.A. COUNTRY: U RESULT 8 US-09-000-041A-1 g g ò ò

TELECOMMUNICATION INFORMATION:

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1718 AAAAAACTTAGAGAGAGAGAGAGAGAATCAAAATAACCTATGAAGATTTATAGAAAAC 1659
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Pred. No. 0.29;
0; Mismatches 62; Indels 0
                                                                                                                                                                                                                                  APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
CORRESPONDENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF-0356 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
                                                                   Sequence 54, Application US/08933750C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PP-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
                                                                                                                                      Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
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Best Local Similarity 54.4%;
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1750 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: Septembe
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                 Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: HMC1NOT01
CLONE: 9476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Con
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                       5932442
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                                                                                                                                                                 APPLICANT:
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APPLICANT:
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                                                                                              ; Patent No.
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Sequence 2083, Application US/09134001C

Sequence 2083, Application US/09134001C

Sequence 2083, Application US/09134001C

GENERAL INFORMATION:

APPLICANT: Lynn boucette-Stamm et al

TITLE OF INVENTION: DETDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

SEQ ID NO 2083

SEQ ID NO 2083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1507 AATGAAAACAATGGACCCTGGCTATCCCAAGCCAATCACAGTCTGGAAAGGGATCCCTGA 1566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1567 ATCTCCTCAGGGAGCATTTGTACACAAAGAAAATGGCTTTACGTATTTCTACAAAGGAAA 1626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           456 TCTTTTGGATTTAGGACACCATGAAAGGTCTATCATGACAGATCTATACTACTTCAGTCA 515
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                                                                                                                                                                                                                                                                                                                                 2.2%; Score 37.6; DB 3; Length 2116; 49.6%; Pred. No. 0.18; ive 0; Mismatches 124; Indels 4
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2083
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                                                                                                           LENGTH: 2116
TYPE: Nucleic acid
STRANDEDRESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 49.6
Matches 126; Conservative
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                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2116
TELEPHONE: 202-721-820
TELEFAX: 202-721-8250
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US-09-140-804-9
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                                                                       APPLICANT: 121, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF-0356 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
                     Sequence 54, Application US/09234613
Patent No. 6132973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAAATGCTTTCCACA 1583
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                                                                                                                                                                                                                                                                                                                        STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compartible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1750 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: HMC1NOT01
CLONE: 9476
                                   Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lal, Pre
APPLICANT: Hillman,
APPLICANT: Bandman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                          USA
US-09-234-613-54/c
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RESULT 12 18-09-140-804-9/c 1 Sequence 9, Application US/09140804 1 Patent No. 6197930

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3947 GGAAGTTGAGTGCGTATGTTATTTTAGACAAAGTAGACTTCAGAACACAGAAAATTATC 3888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3887 ACAGATAAAGAAGGACATTACATAATGATAAGAGAGTAAATGCACCAATAAGACATAATA 3828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3827 CTAAACATGTATATATATAGAGGGCTAAAATATATGAAGCAAAAGCTGACAGAA 3768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 TGGAGCTAAAGAGCTCTGGT-TTTTTCTACAAAGCGAACTGAAGAAATTAAAGCATTTAG 421
                                                                                                                                                                                                                                                                                                                                                                                                                      183 GCGAATGGCTGAGTCTCTCCGAATACCAGAAGGCCCCATTGACCAGGGGACAGCTACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 GAAACAAGCTAGAAATGGTCTGGGGAAGGATCATGAAATCTTAAGAAGGAGGATTGAAAA
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                                                                                                                                                                                                                                                                                                                                       DB 3; Length 4517;
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APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT APPLICATION NUMBER: 60/056,983
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER APPLICATION NUMBER: 60/056,983
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PSELSEQ FOR Windows Version 3.0
SEQ ID NO 9
LENGTH: 4517
                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 200; Indels
                                                                                                                                                                                                                                                                                                                                     2.1%; Score 36; Di 45.4%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                     Query Match 2.13
Best Local Similarity 45.4'
Matches 167; Conservative
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                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Erickson, Mary Ruth
TITE OF INVENTION: OBG3 Giobular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US6.CIP
CURRENT APPLICATION NUMBER: US/09/909,547
CURRENT FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                               3827 CTAAACATGTATATATCTAATAAAGAGGGCTAAAATATATGAAGGAAAAGCTGACAGAA 3768
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Pred. No. 1
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167; Conservative
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Best Local S
Matches 167
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45.4%; Pred. No. 1;
tive 0; Mismatches 200; Indels
 Score 36; DB 4; Length 451
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Query Match 2.1%;
Best Local Similarity 45.4%;
Matches 167; Conservative
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<sup>3827</sup> CTAAACATGTATATATTGTAATAATAGAGGGCTAAAATATATGAAGCAAAAGCTGACAGAA 3768 482 GGTCTATCAŢGACAGATCTAŢĀCTĀCCTÇAĞTCAĀAÇĀGAŢĢGĀGGĞGĀTTGGCĢTG 541 원 ઠે

<sup>542</sup> AAAAAGAG 549 |||||| 3767 CTAAAGAG 3760

Search completed: February 2, 2004, 18:41:15 Job time : 115.569 secs

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February 2, 2004, 12:16:51; Search time 604.522 Seconds (without alignments) 10417.799 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query Match Length DB ID Description

1 1728 10.00 1728 11 US-09-971-773-2 Sequence 2, Appli 3 1498.2 86.7 2100 9 US-09-839-136-9 Sequence 9, Appli 4 140.8 86.7 2100 9 US-09-839-136-9 Sequence 1, Appli 5 1467.8 84.9 1728 9 US-09-839-136-1 Sequence 7, Appli 6 931 53.9 979 11 US-09-839-136-1 Sequence 7, Appli 8 161.8 20.9 41 105-09-971-773-7 Sequence 7, Appli 8 161.8 20.9 42.2 11 US-09-971-773-7 Sequence 7, Appli 8 161.8 20.9 41.2 11 US-09-971-773-7 Sequence 1, Appli 8 161.8 20.9 41.2 11 US-09-971-773-7 Sequence 1, Appli 1 US-09-971-773-7 Sequence 13359, Appli 1 US-09-971-773-7 Sequence 13322, Appli 1 US-09-971-773-7 Sequence 13322, Appli 1 US-09-971-773-3 Sequence 23.44, Appli 1 US-09-971-773-3 Sequence 3, Appli 1 US-09-971-773-3 Sequence 23.44, Appl

Sequence 52289, A Sequence 29920, A	Sequence 33106, A	Sequence 4992, Ap	Sequence 154, App	Sequence 265946,	Sequence 265946,							Sequence 352, App				Sequence 352, App	Sequence 352, App	Sequence 1, Appli	Sequence 40955, A	Sequence 40955, A	Sequence 1, Appli	Sequence 1, Appli	Sequence 115, App	Sequence 6, Appli	ä	ť,	1697	Sequence 2240, Ap
US-10-242-535A-52289 US-09-864-761-29920	US-09-918-995-33106	US-09-908-975-4992	US-08-781-986A-154	US-10-027-632-265946	US-10-027-632-265946	US-10-140-472-352	US-10-141-761-352	US-10-142-885-352	US-10-158-790-352	US-10-137-871-352	US-10-140-805-352	US-10-140-864-352	US-10-140-923-352	US-10-141-756-352	US-10-141-759-352	US-10-123-155-352	US-10-146-731-352	2 US-10-289-762-1	US-10-027-632-40955	US-10-027-632-40955	3 US-10-312-841-1	US-09-734-002-1	US-09-964-824A-115	US-10-142-174-6	2 US-10-419-723-1	5 US-10-067-514-1	US-09-974-300-1697	US-09-998-598-2240
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122.2	85.2	51	42	41.4	41.4	38.6	38.6	38.6	38.6	38.6	38.6	38.6	38.6	38.6	38.6	38.6	38.6	38	37.8	37.8	37.8	37.6	37.6	37.6	37.6	37.6	37	36.8
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US-09-971-773-2

Sequence 2, Application US/09971773

Publication No. US20030115614A1

GENERAL INFORMATION:

APPLICANT: Yutaka KANDA

APPLICANT: Kazuyasu NAKAWURA

APPLICANT: Kazuyasu NAKAWURA

APPLICANT: Kazuyasu NAKAWURA

APPLICANT: Razuyasu NAKAWURA

APPLICANT: Naoko YAMASAKI

APPLICANT: No. US20030115614A1uu HANAI

TITLE OF INVENTION: ANTIBOSY COMPOSITION-PRODUCING CELL

FILE REFERENCE: 249-202

CURRENT FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: US 60/268,926

PRIOR PILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: US 60/268,926

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 73

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 1728

TYPE: DNA

ORGANISM: Mus musculus

US-09-971-773-2

QUELY MATCH

BEST LOCAL SIMILARITY 100.0%; Pred. No. 0;

MAICHES 1728; CONSERVATION O. 0;

MAICHES 1728; OD NO. 0;

ANTOROGRAPHICATION O. 0;

MAICHES 1728; OD NO. 0;

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1 ATGCGGGCATGGACTGGTTCCTGGCGTTGGATTATGCTCATTCTTTTTGCCTGGGGGACC 60	61 TIGITATITITATATAGGIGGICATITIGGITCGAGATAATGACCACCCTGATCACTCCAGC 120	CGAGAACTGTCCCAAGATTCTGGCAAAGCTTGAACGCTTAAAACAGCAGAATGAAGACTTGAGCGAATGGAAGACTTGAAGCCTTGAAACGCCCCATTGACCAGAGGCCCCATTGACCAGAGGCCCCATTGACCAGAGGCCCCATTGACCAGAGGCCCCATTGACCAGAGGCCCCATTGACCAGAGGCCCCATTGACCAGGGGACAGCTACA	378 AGGCGAATGGCCGAATCTCTCGGATACCAGAGGCCCTATTGATCAGGGGCCAGCTATA 437 241 GGAAGGTCCGTGTTTTAGAACAGCTTGTTAAGGCCAAAGAACAGATTGAAATTAC 300 438 GGAAGAGTACGCGTTTTAGAAGAGAGCTTGTTAAGGCCAAAGAACAGATTGAAAATTAC 497	301 AAGAAACAAGCTAGAAATGGTCTGGGGAAGGATCATGAAATCTTAAGAAGGAGGATTGAA 360 	361 AATGGAGCTAAAGAGCTCTGGTTTTTTCTACAAAGCGAACTGAAGAATTAAAGCATTTA 420 	421 GAAGGAAATGAACTCCAAAGACATGCAGAATTCTTTTGGATTTAGGACACCATGAA 480 	481 AGGTCTATCATGACAGATCTATACTCCAGTCAACAGATGGAGGAGGATTGGCGT 540 	541 GAAAAAGGCCAAAGATCTGACAGAGCTGGTCCAGGAGAATAACATATCTCCAGAAT 600 	601 CCTAAGGACTGCAGGAAAGCCAGGAAGCTGGTGTAACATCAATAAAGGCTGTGGCTAT 660 	661 GGTTGTCAACTCCATCACGTGGTCTACTGTTTCATGATTGCTTATGGCACCCAGCGAACA 720 	721 CTCATCTTGGAATCTCAGAATTGGCGCTATGCTACTGGTGGATGGGAGACTGTTTAGA 780 	781 CCTGTAAGTGAGACATGTACAGACAGATCTGGCCTCTCCACTGGACACTGGAGTGAA 840 	841 GTAAATGACAAAACATTCAAGTGGTCGAGGTCCCCATTGTAGACAGCCTCCATCCTCGG 900 	901 CCTCCTTACTACCACTGGCTGTTCCAGAAGACCTTGCAGACGACCGAC	961 GGTGACCTGCAGTGTGGGTGGCTCCCAGTTTGTCAAATACTTGATTCGTCCACAACCT 1020 	1021 TGGCTGGAAAAGGAAATAGAAGGCCCCCAAGAAGCTTGGCTTCAAACATCCAGTTATT 1080 
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TON: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
PA00510.

TION: WINDER: US/10/106,698

DATE: 2002-03-27

ON NUMBER: PCT/US00/26524

TE: 2000-09-29

ON NUMBER: US 60/157,137

TE: 1999-09-29

ON NUMBER: US 60/163,280

ET: 1999-11-03

DO NOS: 8564

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Pred. No. 0;
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                                                    Query Match
Best Local Similarity 91.7%;
Matches 1585; Conservative
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TITLE OF INVENTION: ALPHA 1-6 FUCOSYLTRANSFERASE
FILE REFERENCE: 2356-7
CURRENT APPLICATION NUMBER: US/09/839,136
CURRENT FILING DATE: 2001-04-23
PRIOR PAPLICATION NUMBER: 09/442,629
PRIOR PLING DATE: 1999-11-18
PRIOR PLING DATE: 1999-01-07
PRIOR PLING DATE: 1999-01-07
PRIOR PLING DATE: 1997-01-07
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
SEQ ID NOS: 15
SEQ ID NOS: 15 RESULT 5
US-09-839-136-1
Sequence 1, Application US/09839136
Patent No. US20020081694A1
GENERAL INFORMATION:
APPLICANT: Naoyuki TANIGUCKI et al.

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Pred. No. 0;
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84.9%;
Best Local Similarity 90.6%;
Matches 1565; Conservative
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Pig
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1728)
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Publication No. US20030115614A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mitsuo SATOH
APPLICANT: Kazuyasu NAKAMURA
APPLICANT: Toyohide SHINKAWA
APPLICANT: Toyohide SHINKAWA
APPLICANT: Mocto YAMANE
APPLICANT: No. US20030115614Aluo HANAI
APPLICANT: Mocto YAMASAKI
APPLICANT: No. US2003011561AIluo HANAI
FILE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELLI
FILE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING
CURRENT APPLICATION NUMBER: US/09/971,773

CURRENT FILING DATE: 2002-08-30
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1020 TTGGCTGGAAAAGGAAATAGAAGAAGCCACCAAGAAGCTTGGCTTCAAACATCCAGTTAT 1079
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                                                               TAAAGGTATCAACAGAAAACTTGGAAAAACAGGCTTATATCCCTCCTACAAAGTCCGAGA
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Pred. No. 1.2e-251;
0; Mismatches 53; Indels 0:
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MICHAEN AND APPLICANT: MICHAEN BAPPLICANT: MICHAEN BAPPLICANT: KAZUYASU NAKAMÜRA APPLICANT: KAZUYASU NAKAMÜRA APPLICANT: TOYONIGE SHINKAMA APPLICANT: TOYONIGE SHINKAMA APPLICANT: NGOO YAMAGAKI APPLICANT: NO. US20001156114Aluo HANAI TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL FILE REFERENCE: 249-202 CURRENT FILLING ANTIBODY COMPOSITION-PRODUCING CELL FILE REFERENCE: 249-202 CURRENT FILLING ANTE: 2002-08-30 PRIOR APPLICATION NUMBER: US 60/268,926 PRIOR PILING DATE: 2000-10-06 PRIOR PILING DATE: 2000-10-06 PRIOR FILING DATE: 2001-02-16 NUMBER OF SEQ ID NOS: 73 SEQ ID NO 6 LENGTH: 979
                                                                                                                                             1680 GAAGATAGAAACAGTCAAG 1698
                                                                                                                                                                      GAAGATAGAAACGGTCAAG 979
                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09971773; Publication No. US20030115614A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 51.7%;
Best Local Similarity 94.6%;
Matches 926; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Cricetulus griseus
US-09-971-773-6
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yutaka KANDA
                                                                 1620
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                                                                                                                                                                                                                                              Score 931; DB 11; Length 9
Pred. No. 1.9e-262;
0; Mismatches 30; Indels
PRIOR APPLICATION NUMBER: JP 2000-308526
PRIOR FILING DATE: 2000-10-06
PRIOR PAPLICATION NUMBER: US 60/268,926
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 73
SEGTRARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 979
                                                                                                                                                                                                                                              Luciy match 53.9%;
Best Local Similarity 96.9%;
Matches 949; Conservative
                                                                                                                                                                                     ; ORGANISM: Rattus norvegicus US-09-971-773-7
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GREERL INFORMATION:
APPLICANT: Benn, Sharron G.
APPLICANT: Benn, Sharron G.
APPLICANT: Bark, David R.
APPLICANT: HARE, David R.
APPLICANT: HARE, David R.
APPLICANT: GLOW, Wensher B.
TITLE OF INVENTION: GREER EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GREE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERSNOE: Aeonica-X-1
CURRENT APPLICATION NUMBER: US 60/180,312
RIGH FILING DATE: 2001-65-23
RIGH FILING DATE: 2000-62-46
RIGH FILING DATE: 2000-63-46
RIGH FILING DATE: 2000-63-46
RIGH FILING DATE: 2000-63-46
RIGH RILL APPLICATION NUMBER: US 60/207,456
RIGH RILL APPLICATION NUMBER: US 60/207,466
RIGH RILL APPLICATION NUMBER: US 60/207,666
RIGH RILL APPLICATION NUMBER: PCT/US01/0066
RICH RILL RILL APPLICATION NUMBER: PCT/US01/0066
RICH 1003 1063 1123 1124 CCTTCCACCCCATCGAGGAGTACATGGTACACGTTGAAGAACATTTTCAGCTTCTCGCAC 1183 241 301 302 TCAAACATCCAGTTATTGGAGTCCATGTCAGACGCACAGACAAAGTGGGAAACAGAAAGCTG 361 362 CCTTCCATCCCATTGAAGAGTACATGGTGCATGTTGAAGAACATTTTCAGCTTCTTGCAC 421 ACAGCCTCCATCCTCGGCCTCCTTACCACACTGGCTGTTCCAGAAGACCTTGCAGACC 182 GACTTGTACGAGTGCATGGTGACCCTGCAGTGTGGTGGTGGTGTCTCAGTTTGTCAAATACT 1064 TCAAACATCCAGTTATTGGAGTCCATGTCAGACGCACAGACAAAGTGGGAACAGAAGCAG 1004 TGATTCGTCCACAACCTTGGCTGGAAAAGGAAATAGAAGAAGCCACCAAGAAGCTTGGCT ; Sequence 13359, Application US/09864761 ; Patent No. US20020048763A1 ; GENERAL INFORMATION: G 1184

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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng F.
TITLE OF INVENTION: HUMAN (ENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
US-09-64-761-13292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 13292
LENGTH: 551
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Pred. No. 5.2e-51;
0; Mismatches 62;
                                                                     PRIOR FILING DATE: ZOU1-01-30
PRIOR PELING DATE: ZOU1-01-30
PRIOR APPLICATION NUMBER: FCT/USO1/00668
PRIOR APPLICATION NUMBER: FCT/USO1/00668
PRIOR PILING DATE: Z001-01-30
PRIOR PILING DATE: Z001-01-30
PRIOR APPLICATION NUMBER: FCT/USO1/00662
PRIOR APPLICATION NUMBER: FCT/USO1/00662
PRIOR PILING DATE: Z001-01-30
PRIOR PILING DATE: Z001-01-30
PRIOR PILING DATE: Z001-01-30
PRIOR PELING DATE: Z001-01-30
PRIOR PELING DATE: Z001-01-30
PRIOR PELING DATE: Z000-09-21
PRIOR PELING DATE: Z000-09-31
PRIOR PELING DATE: Z000-09-31
                                                       FILING DATE: 2001-01-30
APPLICATION NUMBER: FCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
12.2%;
Best Local Similarity 80.(%;
Matches 248; Conservative (
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR PILLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILLE REFERENCE: Aeomica-X-1
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 503;
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OTHER INFORMATION: MAP TO ALL09847.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
US-09-864-761-13359
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 13359
LENGTH: 503
                                                                                                                                                                                                                                                                                                                                                                                                                       15.6%; Score 269.2; DB 9;
89.8%; Pred. No. 3.4e-68;
ive 0; Mismatches 33;
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PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
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CURRENT FILING DATE: 2001-05-23
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Patent No. US20020048763A1
GENERAL INFORMATION:
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Best Local Similarity 89.8
Matches 289; Conservative
                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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| APPLICANT: CHEN. WERRAND SHOWE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILTE REPRESENCE: Aconica-X-1 (CHESENT APPLICATION HUMBER: US (0) 864, 761 (CHESENT APPLICATION MUMBER: US (0)160,312 (CHESENT APPLICATION MUMBER: US (0)180,312 (CHESENT APPLICATION MUMBER: US (0)20,456 (CHESENT FILING DATE: 2001-05-23 (CHESENT FILING DATE: 2000-05-20 (CHESENT PRIOR FILING DATE: 2000-05-20 (CHESENT PRIOR FILING DATE: 2000-05-20 (CHESENT PRIOR FILING DATE: 2001-01-30 (CHESENT PRIOR FILING DATE: 2001
                                                                                                                       121 recarecreacecrecacreaceceres and reconstructions and reconstructions are reconstructed as the reconstruction of the reconstructi
                                                                                                                                                                                                                                                                       1016 AACCTTGGCTGGAAAAGGAAATAGAAGAGCCACCAAGAAGCTTGGCTTCAAACATCCAG
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OTHER INFORMATION: MAP TO AL109847.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
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                                       956 TCCATGGTGACCCT
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ORGANISM: Homo sapiens
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NY: EXPRESSED IN FETAL LIVER, SIGNAL = 3.5

NY: EXPRESSED IN PLACENTA, SIGNAL = 4.6

NY: EXPRESSED IN HBL100, SIGNAL = 3.6

NY: EXPRESSED IN HBL100, SIGNAL = 3.6

NY: EXPRESSED IN LUNG, SIGNAL = 5.1

NY: EXPRESSED IN LUNG, SIGNAL = 5.1

NY: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7

NY: EXPRESSED IN HBLA, SIGNAL = 3.3

NY: EXPRESSED IN BONE MARROW, SIGNAL = 2.9

NY: EXPRESSED IN BONE MARROW, SIGNAL = 2.9

NY: SMISSPROT HTT: QYULZT, EVALUE 0.000+00

NY: HIT: AF038280.1, EVALUE 0.000+00
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SEQ ID NO 18181
LENGTH: 248
                                                                          CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PLILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-09-03
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PLILING DATE: 2000-09-27
PRIOR PLILING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
                                            CURRENT APPLICATION NUMBER: US/09/864,761
FILE REFERENCE: Aeomica-X-1
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Best Local Similarity 89.5
Matches 221; Conservative
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ORGANISM: Homo sapiens
PEATURE:
OTHER INFORMATION: MAP TOTHER INFORMATION: EXPRE
OTHER INFORMATION: EXPRE
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COTHER INFORMATION:
US-09-864-761-18181
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Query Match
Best Local Similarity 84.5
Matches 212; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-864-761-1421
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                                                                                                                                                                                                                                                                                                      61 CCCGTCCTCCATATTTACCCTTGGCTGTACCAGAAGACCTCGCAGATCGACTTGTACGAG 120
                                                                                                                                                                                                                                                                                                                                                                              121 AGAGAACTCTCCAAGATTCTTGCAAAGCTTGAACGCTTAAAACAGCAAAATGAAGACTTG 180
                                                                                                                                                                                                                                                                            CTCGGCCTCCTTACTTACCACTGGCTGTTCCAGAAGACCTTGCAGACCGACTCCTAAGAG 955
                                                                                                                                                                                                                                     1 Grgaagrgaaggacaaaaargricaagrggrcgagcrrcccarrgragacagrcrrcarc 60
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EXPRESSED IN BRAIN, SIGNAL = 1.3
SHISSPROT HIT: 09VL27, RVALUE 6.50e+00
EST HUMAN HIT: AM387766.1, EVALUE 0.00e+00
NT HIT: AF038280.1, EVALUE 0.00e+00
                                                                                                                    DB 9; Length 248;
                                                                                                                  11.9%; Score 205.4; DB 9; Length 89.5%; Pred. No. 1.2e-49; ive 0; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Micro SATOH
APPLICANT: Kazuyasu NAKAMURA
APPLICANT: Kazuyasu NAKAMURA
APPLICANT: Tayohide SHINKAWA
APPLICANT: Toyohide SHINKAWA
APPLICANT: Mocko YAMASKI
APPLICANT: Mocko YAMASKI
APPLICANT: Moto YAMASKI
APPLICANT: No. US20030115614Aluo HANAI
TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL
FILE REFERENCE: 249-202
CURRENT FILING APTE: 2002-08-30
PRIOR PILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 73
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Pred. No. 1e-43;
0; Mismatches
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Best Local Similarity 95.6%;
Matches 194; Conservative
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                                                                                                              Query Match
Best Local Similarity 89.5
Matches 221, Conservative
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                                      OTHER INFORMATION: OTHER INFORMATION:
  OTHER INFORMATION:
                                                           ; OTHER INFORMATIC
US-09-864-761-30284
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US-09-971-773-3
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APPLICANT: Palermo, Adam
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
APPLICANT: Steinmann, Kathleen
APPLICANT: Steinmann, Kathleen
APPLICANT: Blias, Josh
APPLICANT: Martens, Maureen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: THERAFY OF BREAST CANCER
FILE REFERENCE: MRI-032
FILE REFERENCE: MRI-032
FILE REFERENCE: MRI-032
CURRENT FILING DATE: 2002-04-19
FRICA PAPLICATION NUMBER: US 60/285,163
FRICA FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 1417
SOFTWARE: Fast SEQ for Windcws Version 4.0
SEQ ID NO 274
LENGTH: 481
2669 AGAGAACTCTCCAAGATTCTTGCAAAGCTGGAGGGCTTAAAACAACAAAAATGAAGACTTG 2728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 CAGGAAGAGTCCGTGJTTTAGAAGAACAGCTTGTTAAGGCCCAAAGAACAG-ATTGAAAAT
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84.5%; Pred. No. 2e-32;
rative 0; Mismatches 33; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature; northing: 128, 402, 424, 462, 470; CCATION: 204, 266, 320, 328, 402, 424, 462, 470; OTHER INFORMATION: n = A,T,C or G
                                                                                                           2729 AGGAGAATGGCTGAGTCTCTCCG 2751
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Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                         ; Sequence 274, Application UE/10125968; Publication No. US20030215865A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
                                                                                 181 AGGCGAATGCCTGAGTCTCCG
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893 ATCCTCGGCCTCCTTACTTACCACTGGCTGTTCCAGAAGACCTTGCAGACCGACTCCTAA 952
                                          953 GAGTCCATGGTGACCCTGCAGTGTGGTGTGTCCCAG 990
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INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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Pred. No. 2e-26;
0; Mismatches 57; Indels 0
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BONE MARROW, SIGNAL = 2.9
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                                                                             CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT PAILICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PLILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/714,203
PRIOR PLILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/714,203
PRIOR PLILING DATE: 2000-06-30
PRIOR PLILING DATE: 2000-06-30
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Best Local Similarity 73.9%;
Matches 161; Conservative
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
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US-09-864-761-1421
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February 2, 2004, 11:54:20; Search time 3711.31 Seconds (without alignments) 11316.242 Million cell updates/sec
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1728
1 atgcgggcatggactggttc.....atcctgaagctgaaaaatag 1728
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM nucleic - nucleic search, using sw model
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AK051811 Mus muscu AK048520 Mus muscu BQ892101 AGENCOURT CB194828 AGENCOURT

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1728 1728 913.2 801.6

Description

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SUMMARIES

7.6 45.6 1066 6.8 43.2 940 6.8 43.2 940 6.8 43.2 940 6.8 43.2 988 6.4 43.2 988 6.4 41.7 855 6.8 40.3 1027 6.8 40.3 1027 6.8 40.3 1027 6.8 40.3 1027 7.2 36.3 10.2 652 8.8 35.2 652 8.8 35.2 652 8.8 35.2 652 8.8 32.9 956 6.8 33.3 752 7.2 35.3 34.3 752 7.2 35.3 34.3 668 6.8 32.9 658 8.8 32.9 658 8.8 32.9 658 8.8 32.9 658 8.8 32.9 658 8.8 32.9 658 8.8 32.9 658 8.8 32.9 573 7.2 33.3 33.3 668 8.8 32.9 573 8.2 30.3 668 8.8 32.9 658 8.8 32.9 573 8.8 30.8 608 8.8 30.8 607 1.8 30.8 608 8.8 30.7 653 1.9 938 8.8 30.8 607 8.2 31.0 653 1.9 938 8.8 30.8 608 8.8 30.7 658 8.8 30.8 608 8.8 30.8 30.8 608 8.8 30.8 608 8.8 30.8 608 8.8 30.8 608 8.8 30.8 608 8.8 30.8 608 8.8 30.8 608 8.8 30.8 608 8.8 30.8 608 8.8 30.8 608 8.8 30.8 608 8.8 30.8 608 8.8 30.8 608 8.8 30.8 608 8.8 30.8 608 8.8 30.8 608 8.8 30.8 608 8.8 30.8 608 8.8 30.8 608 8.8 30.8 60

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             713 GGAAGAGTCCGTGTTTTAGAAGAACAGCTTGTTAAGGCCAAAGAACAGATTGAAAATTAC 772
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                                                                                                                                                                                                                                                                                                                   /note="unnamed protein product; fucosyltransferase 8 (MGD|MG1:1858901, GB|NM_016893, evidence: BLASTN, 99%, match=2175)
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/db_xref="taxon:10090"
/clone="D230003K17"
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Sumi, N., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, M., Ohacaki, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 2766)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the FANTOM Consortium and the RIKEN Genome Exploration Research
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN) Laboratory for Genome Submission

Submission Besearch Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (8-mail:genome-res@ger.riken.go.jp, Fax:81-45-503-922, Fax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://fantom.gsc.riken.go.jp/.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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s; Score 1728; Ib; Pred. No. 0;0; Mismatches
  Query Match 100.0%;
Best Local Similarity 100.0%;
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/clone="inAdE:6389725" |
/lab. host="Dygan: Olfactory epithelium, Vector: |
/clone | i.b="NIH MGC 129" |
/note="Organ: Olfactory epithelium, Vector: |
pCMV-SPORTE. L.cdb, Site 1: EcoRV, Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size unidirectionally. Primer: Oligo dT. Average insert size is a NIH MGC Library." |
// 215 & Constructed by ResGen, Invitrogen Corp. Note: this is a NIH MGC Library." |
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0; Mismatches 4; Indels 1;
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/organish="Mus musculus"
http://image.llnl.gov
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: ReeGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LINL at:
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/db xref="taxon:10090"
/clone="IMAGE30136221"
/lab host="IMAGE30136221"
/lab host="DH10B (plage-resistant)"
/clone lib="NNH MGC 135"
/clone lib="NNH MGC 135"
/note="Vector: pCMVSport6.1; Site 1: EcoRV; Site 2: NotI;
/note="Westor: pCMVSport6.1; Site 1: EcoRV; Site 2: NotI;
/normalized full-length enriched library from pooled mouse embryonic limb, maxilla and mandible, day 12:5, 13:5, 14:5, and 15:5 (size selector: the 0:5-1 kb tragments)
/cloned directionally, priming method: Oligo-dT. CDNA enrichment: >1k bp, Average insert size 1:6k bp.
/normalization (Cot value): 7:5 kb. Priming sequence:
// SACTAGTTCTAGATCGCGAGCGCGCCC(T)3' Tissue contributed by
/normalization (Lot value): 7:5 kb. Priming sequence:
// David Rowe. Library constructed by ResGen, Invitrogen
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AGENCOURT 11259261 NIH MGC 135 Mus musculus cDNA clone IMAGE:30136221 5', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: NDAM0035 row: h column: 22
High quality sequence stop: 658.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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     GCCTCTGCGAACTTCCATTCTTTGGATGACATCTACTATTTTGGAGGCCAAAATGCCCAC
                                                                                1 GGCCTCCTTACTTACCACTGGCTGTTCCAGAAGACCTTGCAGACCGACTCCTAAAAAGTCC
                                                            AATCAGATTGCTGTTTATCCTCACAAACCTCGAACTGAAGAGGAAATTCCAATGGAACCT
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Pred. No. 4.6e-197;
0; Mismatches 9; Indels 1;
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Matches 818; Conserv
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/mol_type="mRNA"
/db_xref:"taxon:9606"
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/db_xref="taxon:9606"
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/tissue_type="hepatocellular carcinoma, cell line"
/tissue_type="hepatocellular carcinoma; line"
/clone lib="NIH MGC 100"
/clone lib="NIH"
/clone lib="NI
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLCM2025 row: p column: 07
High quality sequence stop: 666.
Location/Qualifiers
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0; Mismatches 103;
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al Similarity 89.2%;
880; Conservative
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1 235 c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arriyed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2455 xow: k column: 03
High quality sequence stop: 700.
Location/Qualifiers
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                        DB 13;
                       Score 747.2; DB 13;
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RESULT 7 BX452321

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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BRail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7499.f For more information about this cluster, see
mute: information about this cluster, see
cgi-bin/cluster.cgi?seq=CSOBAG023ZH04 CS02144_1&cluster=7499.f.
Contact: Feng Liang Email: filang@lffetech.com UL:
Contact: Feng Liang Email: filang@lffetech.com UL:
Contact: Feng Liang Email: filang@lffetech.com UL:
Location/Qualifiers
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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                                  LINE) Homo sapiens cDNA
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/cell_line="RAMOS CELL LINE"
/cell_line="RAMOS CELL LINE"
/close_lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="Vector: pGWYSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned ithe Not I and EcoRV sites of the pGWYSPORT 6 vector.
Library was not normalized." 4 others
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BX452321 Homo sapiens B CELLS (RAMOS CELL clone CSODG005YO07 5-PRIME, mRNA sequence. BX452321
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Pred. No. 8.1e-183;
0; Mismatches 86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DG005Y007"
                                                                                                BX452321.1 GI:31026371
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Best Local Similarity 90.3%;
Matches 807; Conservative 0
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   Library constructed
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Pred. No. 8.4e-180;
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Matches 794; Conservative
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.7894821 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6158200
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/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT
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I (bases 1 to 80.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                       GAAGCTTGGCTTCAAACATCCAGTTATTGGAGTCCATGTCAGACGCACAGACAAAGTGGG
                                                                   GAAGCTTGGCTTCAAACATCCAGTTATTGGAGTCCATGTCAGACGCCACAGACAAAGTGGG
                                                                                                                                                                      GCTTCTCGCACGCAGGATGCAAGTGGATAAAAAAAGAGTATATCTGGCTACTGATGATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTP
Tissue Procurement: ATCC/DCTP
Tissue Procurement: ATCC/DCTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAMN13505 row: e column: 17
High quality sequence stop: 641.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6158200"
/tissue_type="melanotic melanoma"
/lab_host="DH10B" (phage-resistant)"
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AGENCOURT 7971158 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6171012 BU184296
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Precourement: ATC

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1538 row: k column: 13

High quality sequence stop: 711.
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1 (bases 1 to 855)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="DH10B (phage-resistant)"
/cone_lb="NIH MGC_67"
/note="Organ: eye; Vcfor: pCMV-SPORT6; Site_l: NotI;
/note=2. Sall; Cloned unidirectionally. Primer: Oligo
Average insert size 1.75 kb. Library constructed by
                                          1103 ACAAAGTGGGAACAGAAGCAGCCTTCCACCCCATCGAGGAGTACATGGTACA-CGTTGAA
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/db_xref="taxon:9606"
/clone="IMAGE:6171012"
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/tissue type="B CELLS (RAMOS CELL LINE)"
/tissue type="B CELLS (RAMOS CELL LINE)"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="Vector: PCMVSPORT 6; 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCMVSPORT 6 vector. Library was not normalized."

184 c 231 g 218 t 5 others
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90
BX429921 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA clone CSODG005YO07 5-PRIME, mRNA sequence.
BX429921
                                                                                                                                                                                                                                                                                                                               Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7499.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAA012ZA08 CSO1114_1&cluster=7499.f.
Contact : Feng Liang Email : fliangelifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAA012ZA08_CSO1114_1.
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/mol_type="mRNA"
/db xref="taxon:9606"
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Matches 811; Conservative
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EST 12-SEP-2002

BU513162 937 bp mRNA linear ES: AGENCOURT\_10116686 NIH\_MGC\_134 Mus musculus cDNA clone

BUS13162 LOCUS DEFINITION

RESULT 11

1049 1109 1169 4, /tissue type="undifferentiated limb"
/lab host="DH10B (phage-resistant)"
/clone\_lab="NH1H\_MGC\_134"
/note="Véctor: pCMV-SPORT6.1.cdb; Site\_1: EcoRV; Site\_2:
Not1; Cloned unidirectionally. Primer: Öligo dT. Average
insert size 1.7 kb. Constructed by ResGen, Invitrogen
corp. Note: 220 c. 204 g 250 t 3 others 749 809 869 989 300 420 120 180 929 240 Mus musculus
Mus musculus
Bukaryota; Metazoù; Chordata; Craniata; Vertebrata; Buteleostomi;
Musmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 93?)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutés of Health, Mammalian Gene Collection (MGC) 9 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@m(il.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrived by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14073 row: g column: 03
High quality sequence stop: 751. GGGAACAGAAGCAGCUTTCCACCCCATCGAGGAGTACATGGTACACGTTGAAGAACATTT TGGCCTCTCCACTGGACACTGGTCAGGTGAAGTAAATGACAAAAAACATTCAAGTGGA 930 AGACCTTGCAGACCGACTCCTAAGAGTCCATGGTGACCCTGCAGTGTGGTGGTGTGTCCCA 241 AGACCTTGCAGACCGACTCCTAAGAGTCCATGGTGACCCTGCAGTGTGGTGGTGTCCCA GTTTGTCAAATACTTGATTCGTCCACAACCTTGGCTGGAAAAGGAAATAGAAGACCAC 301 GTTTGTCAAATACTTGATTGGTCCACAACCTTGGCTGGAAAAGGAAATAGAAGAAGCCAC 361 CAAGAAGCTTGGCCTTCAACATCCAGTTATTGGAGTCCATGTCAGACGCACAGAAAGT þe 690 TTTCATGATTGCTTA\(\)GGCACCCCAGCGAACACTCATCTTGGAATTTGGCGCTA 1 rrrcargarracerrangecacceaeceaecacrearcressaarcreagaarragececra 810 TGGCCTCTCCACTGGACACTGGTCAGGTGAAGTAAATGACAAAAACATTCAAGTGGTCGA GCTCCCCCATTGTAGA(AGCCTCCATCCTCGGCCTCCTTACTTACCTGCTGGTTCCAGA CAAGAAGCTTGGCTTCAACATCCAGTTATTGGAGTCCATGTCAGACGCACAGACAAAGT Gaps 72; 40.8%; Score 704.6; DB 13; Length 937; llarity 91.4%; Pred. No. 7.8e-172; Conservative 0; Mismatches 5; Indels 72; /organism="Mus musculus" /mol\_type="mRNA" /db\_xrefe"taxon:10090" /clone="iMAGE:6508154" BU513162.1 GI:22820688 al Similarity 819; Conserv Unpublished 1110 셤

Tue Feb

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834\ bp mRNA linear EST 01-AUG-2002 NT2RM2 Homo sapiens cDNA clone NT2RM2001714 5', mRNA
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(Acil line="RAMOS CELL LINE"

/colone lib="Home saplers B CELLS (RAWOS CELL LINE)"

/note="Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dr) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Contact the Not I
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
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BX450010 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens CDNA clone CS0DG005Y007 5-PRIME, mRNA sequence.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
Inbrary was constructed by Life Technologies, a division of
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Library was constructed by Life Technologies, a division of
Http://www.genoscope.cns.fr/
cogi-bin/cluster.orgi?seq=CS0AS0092B00QPl&cluster=7499.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0AS009ZB08QPl.
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     GGGAACAGAAGCAGCCTTCCACCCCATCGAGGAGTACATGGTACACGTTGAAGAACATTT
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/mol_type="mRNA"
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/clone="CSODG005Y007"
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/cell_line="NT2"
/clone_lib="NT2RM2"
/note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal
precursor cells"
187 c 181 g 215 t 2 others
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                                                                                                     HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
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              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 834)
                                                                                                                                                            Contact: Takao Isogai
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomicsehrico.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                     Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
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0; Mismatches 78;
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Best Local Similarity 90.4%;
Matches 744; Conservative 0
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/tissue_incomparation, gross tissue"
/dev stage="5" months"
/lab_host="DH108"
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/clone lib="NLC GAAP Mam4"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
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/note="Organ: pcmv-s
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musculus cDNA clone IMAGE:4978383 5',
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://inage.llnl.gov

Plate: LLAM10974 row: n column: 16

High quality sequence stop: 694.
481 ICCTAGIGIGIATACITITICALCCCAGGICTGTGGGGTTGCTTAIGAAAITAIGCAACAC
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Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
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/clone="%MAGE:4978383"
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/strain="NMRI"
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Laboratory of Genetics
National Institutes of Health
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
Email: cana@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4K.html for details.
Plate: H4019 row: B column: 10
Seq primer: -21M13 Reverse
Pligh quality sequence stop: 656
POLYA=NO.
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/lab_host="DH10B"
/clone_lib="NIA Mouse 7.4K cDNA Clone Set"
/note="Wector: pSPORT1; Site_1: Sal1; Site_2: Not1; This clone is among a rearrayed set of 7,407 clones from more than 20 cDNA libraries."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 CCATGTCAGACGCACAGACAGAGAACAGAACAGCCTTCCACCCATCGAGGAGTA
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38.0%; Score 656; DB 13; L
Best Local Similarity 100.0%; Pred. No. 2.9e-159;
Matches 656; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                        1. 656
/organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6"
/db_xref="missT:H4019B10-5"
/db_xref="taxon:10090"
/clone="H4019B10"
                                                                                                                                                                                                                        Location/Qualifiers
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                                                         AAAATTACAAGAAACAAGCTAGAAATGGTCTGGGGAAGGATCATGAAATCTTAAGAAGGA
                                                                                          4 AAATTACAGAGAAACAAGCTAGAAATGGTCTGGGGAAGGATCATGAAATCTTAAGAAGGA
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Pred. No. 2.4e-160;
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February 2, 2004, 08:39:39; Search time 38.5 Seconds (without alignments) 2370.592 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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                                   Copyright
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Antibody productio	Antibody productio	Human alpha 1-6 fu	Alpha1,6-fucosyl t	Pig alpha 1-6 fuco	Human colon cancer	Human alpha 1-6 fu	Drosophila melanog	Human alpha 1-6 fu
SUMMAKIES			QI .	. ~.	ABG34136	AAW22125	ABB08405	AAW22124	AAG73884	AAB75061	ABB59117	AAB75062
			DB	23	23	18	23	18	22	22	22	22
,			re Match Length DB I	575	575	575	575	575	515	339	619	233
	æ	Query	Match	100.0	98.1	6.96	96.9	93.6	85.7	57.5	48.3	38.7
			Score	3081	3024	2984	2984	2885	2639	1771	1489.5	1193
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WPI; 2002-340182/37.

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## ALIGNMENTS

Antibody production, cytostatic; immunomodulator; vasotropic; virucide; antibacterial; antiinflammatory; antiallergic; allergy; inflammation; autoimmune disease; Chinese hamster ovarian tissue-originated cell; CHO; tumour; circulatory disease; infection. Yamane N; Uchida K, Shinkawa T, , Hanai N; Antibody production method related protein #1. ABG34135 standard; Protein; 575 AA Nakamura K, U , Yamasaki M, (KYOW ) KYOWA HAKKO KOGYO KK. 05-OCT-2001; 2001WO-JP08804. 06-OCT-2000; 2000JP-0308526. 15-JUL-2002 (first entry) Satoh M, N Yamano K, Cricetulus griseus. WO200231140-A1. 18-APR-2002. Kanda Y, S Hosaka E, ABG34135; ABG34135  Antibody production; cytostatic; immunomodulator; vasotropic; virucide; antibacterial; antiinflammatory; antiallergic; allergy; inflammation; autoimmune disease; Chinese hamster ovarian tissue-originated cell; CHO; tumour; circulatory disease; infection.

WO200231140-A1. musculus

Mus

Antibody production method related protein #1

15-JUL-2002 (first entry)

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Cells producing antibody compositions including antibody fragments and fusion proteins with Fc domain of antibody, useful for prevention or treatment of cancer, immune diseases, circulatory diseases and
                                                                                                                                                                                                                                                   accompanying tumour, allergy or inflammation, autoimmune diseases, circultatory diseases, and viral and bacterial infections. The antibodies can be stably produced using the method of the invention with high binding activity and potency thus leading to high safety and reduced side effects when applied alone or in combination with other drugs for therapy. The present sequence represents a protein molecule used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MRAWIGSWRWIMLILFAWGTLLFYIGGHLVRDNDHPDHSSRELSKILAKLERLKQQNEDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEREIEETTKKLGFKHPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to novel method for antibody production comprising a Chinese hamster ovarian tissue-originated (CHO) cell transferred with a gene encoding an antibody molecule for producing a composition comprising an antibody molecule with an FC domain bonded to the N-glycoside linkage complex sugar chain. The produced antibody compositions are drugs for prevention or treatment of diseases
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100.0%; Pred. No. 5.5e-272;
iive 0; Mismatches 0;
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                                                                                                 Claim 23; Page 18-21; 314pp; Japanese
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Best Local Similarity 100.
Matches 575; Conservative
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ABG34136 standard; Protein; 575

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97.6%; Pred. No. 8.8e-267;
tive 9; Mismatches 5;
                                                                                                                                                                                                                                                                                                      Nakamura K, Uchida K,
Yamasaki M, Hanai N;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 33; Page 21-23; 314pp; Japanese
                                                                                                                                                                                                                                                                           (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                       05-OCT-2001; 2001WO-JP08804.
                                                                                                                                                                                                                                                 06-OCT-2000; 2000JP-0308526.
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Yamano K,
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Hosaka E,
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                                                                         GVHVRRTDKVGTEAAFHPIEEYWHVEEHFQLLARRMQVDKKRVYLATDDPTLLKEAKTK
                                                                                                                 YSNYEFI SDNSI SWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIMQ
                                                                                                                                      YSNYBFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIMQ
                                                                                                                                                                                        THPDASANFHSLDDIYYFGGQNAHNQIAVYPHKPRTEBEIPMEPGDIIGVAGNHWDGYS
 PPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEREIEETTKKLGFKHPVI
               GVHVRRTDKVGTEAAFHPIEEYMVHVEEHFQLLERRMKVDKKRVYLATDDPSLLKEAKTK
                                                                                                                                                                           TLHPDASANFHSLDDIYYFGGQNAHNQIAVYPHQPRTKEEIPMEPGDIIGVAGNHWNGYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha 1-6 fucosyltransferase; enzyme; pig; human; fucose transfer; guanosine diphosphate; sugar chain synthesis; modification; antibody; GlcNAc; cancer diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human or pig alpha 1-6 fucosyl:transferase and DNA encoding it - synthesis and modification of sugar chains and used as an antigen for production of diagnostic antibodies
                                                                                                                                                                                                                                    KGVNRKLGKTGLYPSYKVREKIETVKYPTYPEAEK 575
                                                                                                                                                                                                                                                  Uozumi N, Yanagidani S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 39-43; 61pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                              Human alpha 1-6 fucosyltransferase.
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96JP-0010365.
96JP-0161648.
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N-PSDB; AAT76574.
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21-JUN-1996;
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     enzyme is useful in the synthesis and
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in the presence of 5 mM NDTA. The enzyme is useful in the synthesis an modification of sugar chains, and as antigen for the production of antibodies recognising the enzyme. The antibodies can be used for the diagnosis of cancer and other diseases.
                                                                                                                                              1 MRAWIGSWRWIMLILFAWGILLFYIGGHLVRDNDHPDHSSRELSKILAKLERLKQQNEDL
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                                                                                          Length 575;
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                                                                                             DB 18;
                                                                                            96.3%; Score 2984; DB 18; 96.2%; Pred. No. 3.9e-263; ive 10; Mismatches 12;
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                                                                                                         Best Local Similarity 96.29
Matches 553; Conservative
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                                                                                                                                                                                                                    The invention relates to a plant cell with an animal type sugar chain adding function, created by transforming a tobacco cell with a gene encoding an enzyme derived from an animal which can transfer a fucose residue to the reductive end acetylglucosamine residue of a sugar chain. The gene that is introduced into the plant cell encodes the enzyme alphal, 6-fucosyl transferase. The method of the invention is useful for the preparation of a glycoprotein having animal type sugar chain. The current sequence represents alphal, 6-fucosyl transferase amino acid
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                                                                                                                                          A plant cell with an animal type sugar chain adding function, preparation of a glycoprotein with an animal type sugar chain
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                                                                                                                                                                                          Example 1; Page 24-26; 38pp; Japanese
22-MAR-2000; 2000JP-0081059
                                TANIGUCHI N
                                                                                            WPI; 2002-158816/21
                                                              FUJIYAMA K.
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Lucosyltransferases of the invention, respectively. The enzyme transfers fucosyltransferases of the invention, respectively. The enzyme transfers fucosyltransferases of the invention, respectively. The enzyme transfers fucosyltransferases of the invention, respectively. The enzyme transfers concerned against and against a followable for the 6-hydroxyl group of the GlcNAccern areases 1-2Manalpha 1-6) [GlcNAcbeta 1-2Manalpha 1-6] [GlcNAcbeta 1-4GlcNAc-R 1 thas an optimum ph of about 1-4GlcNAcbeta 1-4 [Fucalpha 1-6) [GlcNAc-R. It has an optimum ph of about 1-6 [GlcNAc-R. It has an optimum ph of about 1-6 [GlcNAc-R. It has an optimum ph of about 1-6 [GlcNAc-R. It has an optimum ph of about 1-6 [GlcNAc-R. It has an optimum ph of about 1-6 [GlcNAc-R. It has an optimum ph of about 1-6 [GlcNAc-R. It has an optimum ph of about 1-6 [GlcNAc-R. It has an optimum ph of about 1-6 [GlcNAc-R. It has an optimum ph of about 1-6 [GlcNAc-R. It has an optimum ph of about 1-6 [GlcNAc-R. It has an optimum ph of about 1-6 [GlcNAc-R. It has an optimum ph of about 1-6 [GlcNAc-R. It has an optimum ph of about 1-6 [GlcNAc-R. It has an useful in the synthesis and 1-6 [GlcNAc-R. It has an optimum ph of about 1-6 [GlcNAc-R. It has 1-6 [GlcNAc-
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synthesis and modification of sugar chains and used as an antigen
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                                                                         Pig alpha 1-6 fucosyltransferase.
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96JP-0010365.
96JP-0161648.
96JP-0162813.
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(first entry)
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Best Local Simil
Matches 534; C
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LALESHWWRYATGGWETVFRPVSETCTDRSGSSTGHWSGEVKDKNVQVVELPIVDSVHPR
                                                                                                                    ALHPDASANFRSLDDIYYFGGPNAHNQIAIYPHQPRTEGEIPWEPGDIIGVAGNHWDGYP
                                                                    PPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEREIEETTKKLGFKHPVI
                                                                               PPYLPLAVPEDLADRLVRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVI
                                                                                                          GVHVRRTDKVGTEAAFHPIEEYMVHVEEHFQLLERRMKVDKKRVYLATDDPSLLKEAKTK
                                                                                                                                                 YSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIMQ
                                                                                                                                                           TLHPDASANFHSLDDIYYFGGQNAHNQIAVYPHQPRTKEEIPMEPGDIIGVAGNHWNGYS
                                                                                                                                                                                                                                                                                                                                                                                 colon cancer; colon cancer antigen; diagnosis; detection;
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99US-0163280,
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N-PSDB; AAH33315.
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03-NOV-1999;
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Additionally, N may be used to produce the colon cancer-associated Ps, Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
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11; Mismatches 11;
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Best Local Similarity 95.7%
Matches 489; Conservative
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alpha 1-6 fucose
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                                                                                                                                                                                                                                                                                                                                                                           EIMQTLHPDASANFHSLDDIYYFGGQNAHNQIAIYAHQPRTADEIPMEPGDIIGVAGNHW 300
                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                         fucosyltransferase (alpha 1-6 fuct, also called alpha 1-6 fucose transferase) antibody. Also described are: (1) a hybridoma producing the above monoclonal antibody; (2) an immunoassay for detecting human alpha 1-6 fuct by using the above antibody or its antibody fragment; and (3) a reagent used for the above immunoassay. The anti-human alpha 1-6 fuct antibody can be used for immunoassay. The present sequence represents the human alpha 1-6 fuct protein of residues 237 to 575, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                   1 TQRTLILESQNWRYATGGWETVFRPVSETCTDRSGISTGHWSGEVKDKNVQVVELPIVDS
                                                                                                                                                                                                                                                                                                                                                                                                                     121 HPVIGVHVRRTDKVGTEAAFHPIEEYMVHVEEHFQLLARRMQVDKKRVYLATDDPSLLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKTKYPNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFISQADFLVCTFSSQVCRVAY
                                                                                                                                                                                                                                                                                                                       237 TQRTLILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVKDKNVQVVELPIVDS
                                                                                                                                                                                                                                                                                                                                                                LHPRPPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEREIBETTKKLGFK
                                                                                                                                                                                                                                                                                                                                                                                                          HPVIGVHVRRTDKVGTEAAFHPIEEYMVHVEEHFOLLERRMKVDKKRVYLATDDPSLLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKTKYSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIMQTLHPDASANFHSLDDIYYFGGQNAHNQIAVYPHQPRTKEEIPMEPGDIIGVAGNHW
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                              for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                              Length 339;
                                                                                             anti-human alphal-6 fucose transferase antibody useful
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                  present invention describes an anti-human alpha 1-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGYSKGVNRKLGRTGLYPSYKVREKIETVKYPTYPEAEK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGYSKGVNRKLGKTGLYPSYKVREKIETVKYPTYPEAEK 575
                                                                                                                                                                                                                                                                            Query Match 57.5%; Score 1771; DB 22; Best Local Similarity 96.2%; Pred. No. 8.9e-153; Matches 326; Conservative 8; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ
                                                                                                                             Example 2; Page 8-9; 11pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABBS9117 standard; Protein; 619
 99JP-0183569
                    99JP-0183569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
                                         (FJRE ) FUJIREBIO KK
                                                              2001-275926/29
                                                                                                                                                                                                                                                         339 AA;
                                                                         N-PSDB; AAF87952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical
                      29-JUN-1999;
 29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila;
                                                                                                           immunoassay
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                                                                                                                                                                                                                                                                                                                                                                 297
                                                                                                                                                                                                                                                          Sequence
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ABB59117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---NYKKQARNDL------GKDHEILRRRIENGAKELWFFLQSELKKLKKL--- 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention i useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention signistrations in higher eukaryotes for the development of discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 379 IEEYMVHVEEHFQLLERRMKVDKKRVYLATDDPSLLKEAKTKYSNYEFISDNSISWSAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --EGNELORHADEILLDLGHHERSIMTDLYYLSQTDGAGEWREKEAKDLTELVQRRITYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ONPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQNWRYATGGWETV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRPVSETCTDRSGLSTGHWSGEVKDKNVQVVELPIVDSLHPRPPYLPLAVPEDLADRLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VHGDPAVWWVSQFVKYLIRPQPWLEREIEETTKKLGFKHPVIGVHVRRTDKVGTEAAFHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIMQTLHPDASANFHSLDDIYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 AWTGSW-RWIMLILPAWGTLLFYIGGHLVRDN-----DHPDHSSRELSKILAKLERLKQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 NEDLRRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIE---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425 VEEYMTYVEDYYRTLEVNGSTVARRIFLASDDAQVIEEARRKYPQYQIIGDPEVARMASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 4143; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.1%; Score 1489.5; DB 22; Lengt 46.6%; Pred. No. 1.1e-126; vative 110; Mismatches 168; Indels
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                                                                                                                                                                                                    Myers
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                                                                                                                                                                                                 PWD,
                                                        23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                              Adams M,
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Matches 285; Conserv
                                                                                                                                           (PEKE ) PE CORP NY
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127

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340
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                   RESULT 10
ABG48804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           343 EREIEETTKKLGFKHPVIGVHVRRTDKVGTEAAFHPIEEYWVHVEEHFQLLERRMKVDKK 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
           S45 YGGONAHNRRVVIAHKPRTHEDLQLRVGDLVSVAGNHWDGNSKGKNTRTNQGGLFPSFKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                fucceyltransferase (alpha 1-6 fuct, also called alpha 1-6 fucose transferase) antibody. Also described are: (1) a hybridoma producing the above monoclonal antibody; (2) an immunoassay for detecting human alpha 1-6 fuct by using the above antibody or its antibody fragment; and (3) a reagent used for the above immunoassay. The present sequence represents the human alpha 1-6 fuct methody can be used for immunoassay. The present to sequence represents the human alpha 1-6 fuct protein of residues 343 to 575, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVYLATDDPSLLKEAKTKYPNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVCTFSSQVCRVAYEIMQTLHPDASANFHSLDDIYYFGGQNAHNQIAVYPHQPRTKEEIP
FGGONAHNOIAVYPHQPRTKEEIPMEPGDIIGVAGNHWNGYSKGVNRKLGKTGLYPSYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVYLATDDPSLLKEAKTKYSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                              fucosyltransferase; alpha 1-6 fucT; antibody;
transferase; anti-human alpha 1-6 fucT; immunoassay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEPGDIIGVAGNHWDGYSKGVNRKLGRIGLYPSYKVREKIETVKYPTYPEAEK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEPGDIIGVAGNHWNGYSKGVNRKLGKTGLYPSYKVREKIETVKYPTYPEAEK 575
                                                                                                                                                                                                                                                                                                                                                                                      Novel anti-human alpha1-6 fucose transferase antibody useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                           Human alpha 1-6 fucosyltransferase protein 343-575 SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         invention describes an anti-human alpha 1-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1193; DB 22;
Pred. No. 2.8e-100;
6; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 9-10; 11pp; Japanese,
                                                                                                               AAB75062 standard; Protein; 233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.7%;
95.3%;
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                                                                                                                                                                                                                                                                                                              99JP-0183569
                                                                                                                                                       (first entry)
                                                            616
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                                         559 REKIETVKYPTY
                                                            EEKVDTAKLPLY
                                                                                                                                                                                                                                                                                                                                    (FJRE ) FUJIREBIO KK.
                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-275926/29.
N-PSDB; AAF87953.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 AA;
                                                                                                                                                                                               Human; alpha 1-6
alpha 1-6 fucose
                                                                                                                                                                                                                                                  JP2001011097-A.
                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                            29-JUN-1999;
                                                                                                                                                                                                                                                                                                                29-JUN-1999;
                                                                                                                                                        20-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                   immunoassay
                                                                                                                                                                                                                                                                       16-JAN-2001
499
                                                            605
                                                                                                                                   AAB75062;
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339
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Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia, hypercholesterolaemia, coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived sinjle exon nucleic acid probes useful analysing gene expression in human adult liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from WIPO at ftp.wipo.int/pub/published pct sequences.
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Pred. No. 2e-31;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; SEQ ID No 27452; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W, Rank DR;
                                                                                                                                                               Human liver peptide, SEQ ID No 27452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PWLEREIEETTKKLAFKHPVIG 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000, 2000US-0180712.
26-MAY-2000, 2000US-0207456.
30-UJN-2000, 2000US-0608408.
03-AUG-2000, 2000US-0533468.
21-SEP-2000, 2000US-0234687.
27-SEP-2000, 2000US-023459.
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96.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-488898/53.
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                                                                                                                                                                                                                                                                                                                                                               WO200157273-A2.
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                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                           25-FEB-2003
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ABB28797

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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                             Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                     Peptide #1491 encoded by human foetal liver single exon probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.0%; Score 431; DB 22; Length 82; 96.3%; Pred. No. 2e-31; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W, Rank DR
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                                                           ABB33985 standard; Peptide; 82 AA.
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2000US-0207456.
2000US-0608408.
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2000US-0234687.
2000US-0236359.
2000GB-0024263.
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Les 79; Conserv
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for expression analysis is useful for gene the toxicity of chemical expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The probe of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                         Peptide #1448 encoded by breast cell single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from humar breast, comprises number of single exon nucleic acid probes
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                                                                                                                                                                   Human; microarray; single exon probe; gene expression; breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; SEQ ID NO 11765; 327pp + sequence listing; English.
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96.3%; Pred. No. 2e-31;
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ABB28797 standard; Peptide; 82 AA.
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2000US-0608408.
2000US-0632366.
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04-OCT-2000; 2000GB-0024263
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                                                                               (first entry)
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Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 AA;
                                                                                                                                                                                         disease; cancer.
                                                                                                                                                                                                                                                                           WO200157271-A2.
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03-AUG-2000;
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microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
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                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21355-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.

hypertension, cardiac arrhythmias and congenital heart disease, specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expressed single exon probe encoded protein SEQ ID NO: 26852
          Protein #1421 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                     Single exon nucleic acid probes for analyzing gene expression in human hearts -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                 Human, gene expression, heart, microarray, vascular system;
cardiovascular disease, hypertension, cardiac arrhythmia,
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Pred. No. 2e-31;
2; Mismatches 1; Indels
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PWLEKEIEEATKKLGFKHPVIG 82
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2000US-0236359.
2000GB-0024263.
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96.3%;
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2000US-0608408.
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                                                       congenital heart disease
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27-SEP-2000;
                                                                                 Homo sapiens
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280 EVKDKNVQVVELPIVDSLHPRPPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQ 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimar's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon nucleic acid probes for analyzing gene expression in human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of single exon nucleic acid
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Pred. No. 2e-31;
2; Mismatches 1; Indels
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26-MAY-2000, 2000US-0207456.
30-UIN-2000, 2000US-0608408.
03-AUG-2000, 2000US-0532366.
21-SEP-2000, 2000US-0234687.
27-SEP-2000, 2000US-0234687.
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Matches 79; Conservative
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epilepsy; cancer
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Query Match
14.0%; Score 431; DB 22; Length 82;
Best Local Similarity 96.3%; Pred. No. 2e-31;
Matches 79; Conservative 2; Mismatches 1; Indels

us-09-971-773-23.rai

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COMPUTER: AEAJABLE FORM:
COMPUTER: 18M FC compatible
COMPUTER: 18M FC compatible
COMPUTER: 18M FC compatible
COMPUTER: 18M FC compatible
COMPUTER: NordPerfect 6.1 Windows
SOFTWARE: WordPerfect 6.1 Windows
APPLICATION DATA: US/08/913,805A
FILING DATE: 7 JAN 1998
CLASSIFICATION: 435
PRICA APPLICATION DATA: PP 19260
FILING DATE: 23 JAN 1997
APPLICATION NUMBER: PP 19260
FILING DATE: 22 JUL 1996
APPLICATION NUMBER: JP 162813
FILING DATE: 22 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JAN 1996
ATTICKNEY/AGENT INFORMATION:
NAME: TOFFENERIC! JUGICH L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 335/31
FELECOMMUNICATION NUMBER: 335/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
TOPOLOGY: linear
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TELEFAX: 202-429-0796
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3+ Flop
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Sequence 12, Appl
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
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2, Appli
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Sequence 1056, Ap
Sequence 17, Appl
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                                                                                                  (without alignments)
1569.596 Million cell updates/sec
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Sequence 10, Appl
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                                                                                   ; Search time 15.5 Seconds
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1 MRAWTGSWRWIMLILFAWGT.....YKVREKIETVKYPTYPEAEK
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RecTUMS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUMS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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US-09-442-629-12
US-09-442-629-12
US-09-104-324B-4
PCT-US96-08950-2
PCT-US96-09127-2
US-08-630-915A-221
US-09-914-259-27
US-08-353-700-1
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US-09-107-149-17
US-09-141-206-6
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US-09-141-206-2
US-08-328-254-6
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Maximum Match 100%
Listing first 45 summaries
                                                                                   February 2, 2004, 08:39:43
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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4, Appli
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5178, Ap
4, Appli
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Sequence 35,
Sequence 19,
Sequence 2, A
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Sequence 517,
Sequence 4,
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Sequence 3
Sequence 3
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APPLICANT: TANIGUCHI, Nacfumi
APPLICANT: UOZUMI, Nacfumi
APPLICANT: SHIBA, Teteroo
APPLICANT: YANGIDANI, Shusaku
TITLE OF INVENTION: Alpha 1-6 Fucosyltransferase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREPT: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
         US-08-701-005A-2
US-08-479-895-2
PCT-US95-02058-2
PCT-US95-02058-4
US-08-91-805A-3
US-09-442-629-3
US-09-914-259-26
US-09-144-011-5178
US-09-144-011-5178
US-09-536-224-4
US-09-536-224-4
US-09-536-224-4
US-08-968-542-35
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US-08-968-542-35
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US-08-968-752B-2
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                      106.5
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RRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIENYKKQARNDLGKDHEILRRRIE
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                                                             APPLICATION NUMBER: PCT/JD97/00171
FILING DATE: 23 JAN 1997
APPLICATION NUMBER: D19260
FILING DATE: 23 JUL 1996
APPLICATION NUMBER: JP 162813
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 21 JAN 1996
                              APPLICATION NUMBER: US/08/913,805A
FILING DATE: 7 JAN 1998
6291219-1999
                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NIWBER: 39,048
REFERRNCE/DOCKET NUMBER: 2356/3
                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-442-629-10
                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEBHONE: 202-429-176
TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 575 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
   FILING DATE:
APPLICATION
                    PRIOR
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                                                                                                                    1 MRAWIGSWRWIMLILFAWGTLLFYIGGHLVRDNDHPDHSSRELSKILAKLERLKQQNEDL
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STREET: 1025 Connecticut Avenue, N.W.,
CITY: Washington
STATE: DC
                                                   96.9%; Score 2984; DB 3; 96.2%; Pred. No. 6.1e-270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: 3+ Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WordPerfect 6.1 Windows
                                                                                  10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/442,629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: TANIGUCHI, Naoyuki UOZUMI, Naobumi SHIBA, Tetsuo YANAGIDANI, Shusaku TITLE OF INVENTION: Alpha 1-6 Fu NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09442629
Patent No. 6291219
GENERAL INFORMATION:
                                               Query Match 96.9%;
Best Local Similarity 96.2%;
Matches 553; Conservative
   peptide
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   MOLECULE TYPE:
      ; MOLECULE TYPI
US-08-913-805A-10
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181 EKEAKDLTELVORRITYLQNPKDCSKAKKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRT 240
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SHIBA, Tetsuo
YANAGIDANI, Shusaku
TITLE OF INVENTION: Alpha 1-6 Fucosyltransferase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541 KGVNRKLGRTGLYP&YKVREKIETVKYPTYPBADK 575
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FILING DATE: 7 JAN 1998
APPLICATION NUMBER: PCT/1997/00171
FILING DATE: 23 JAN 1997
APPLICATION NUMBER: JP 19260
FILING DATE: 23 JUL 1996
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 161813
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 23 JUN 1996
APPLICATION NUMBER: JP 101658
FILING DATE: 24 JAN 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WordPerfect 6.1 Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/442,629
FILING DATE: 10.NO. 6291219-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 39,048
REFERENCE/DOCKUT NUMBER: 2356/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 + Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Toffenetti, Judith L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: TANIGUCHI, Naoyuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/09442629; Patent No. 6291219; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1025 Connecticut Avenue, N.W., Suite 600 CITY: Washington STATE: DC
                                                                                                                                                                                                          APPLICANT: TANIGUCHI, Naoyuki
APPLICANT: TANIGUCHI, Naofumi
APPLICANT: SHIBA, Tetsuo
APPLICANT: YANAGIDANI, Shusaku
APPLICANT: YANAGIDANI, Shusaku
TITLE OF INVENTION: Alpha 1-6 Fucosyltransferase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: 3+ Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WORDPEFfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/913,805A
FILING DATE: 7 JAN 1998
CLASSIFCATION *435
PRIOR APPLICATION NUMBER: PCT/JP97/00171
FILING DATE: 23 JAN 1997
APPLICATION NUMBER: UP 162813
FILING DATE: 22 JUL 1996
APPLICATION NUMBER: UP 162813
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: UP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: UP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: UP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: UP 10365
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: UP 10365
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: UP 10365
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: UP 10365
FILING DATE: 24 JAN 1996
ANAMP: CFÉGNET: ANAMP: TOÉGNET: ANAMP: CFÉGNET: ANAMP: TOÉGNET: ANAM
                                                                                                                        Sequence 2, Application US/08913805A Patent No. 6054304 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Toffenetti, Judith L. REGISTRATION NUMBER: 39,048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 202-429-1776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 575 amino acids
amino acid
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Matches 534; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino ació
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                   481 TLHPDASANFHSLDDJYYFGGQNAHNQIAVYPHQPRTKEEIPMEPGDIIGVAGNHWNGYS 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 ALHPDASANFRSLDDIYYFGGPNAHNQIAIYPHQPRTEGEIPMEPGDIIGVAGNHWDGYP 540
241 LALESHNWRYATGGWETVFRPVSETCTDRSGSSTGHWSGEVKDKNVQVVELPIVDSVHPR 300
                                                                                                                                                                                         361 GVHVRRIDKVGTEAAFHPIEEYMVHVEEHFQLLERRMKVDKKRVYLATDDPSLLKEAKTK 420
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                                                                              301 PPYLPLAVPEDLADRILLRVHGDPAVWWVSQFVKYLIRPQPWLEREIEETTKKLGFKHPVI
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NGAKELWFFLOSELKKLKNLEGNELORHADEFLSDLGHHERSIMTDLYYLSQTDGAGDWR 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 LILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVKDKNVQVVELPIVDSLHPR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 PPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEREIEETTKKLGFKHPVI 360
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                                                                                                                                                                                                                                                                                             1 MRAWIGSWRWIMLILFAWGTLLFYIGGHLVRDNDHPDHSSRELSKILAKLERLKQQNEDL
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                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                      Length 575;
                                                                                                                                                                                                                                                Indels
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Sequence 12, Application US/08913805A

BREAL INFORMATION:
APPLICANT: TANICUCHI, Nacyuki
APPLICANT: SHIBA, Tetsuo
APPLICANT: SHIBA, Tetsuo
TITLE OF INVENTION: Albha 1-6 Fucosyltransferase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
STATE: DC
COUNTRY: US
ZCOUNTRY: SADABLE FORM:
                                                                                                                                                                                                    Query Match 93.6%; Score 2885; DB 3; I
Best Local Similarity 92.9%; Pred. No. 1.1e-260;
Matches 534; Conservative 16; Mismatches 25;
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                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TANIGUCHI, Naoyuki
UOZUMI, Naofumi
SHIBA, Tetsuo
YANAGIDANI, Shusaku
TITLE OF INVENTION: Albha 1-6 Fucosyltransferase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
4.3%; Score 131; DB 3; I
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 3+ Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-05/MS-DOS 6.2
SOFTWARE: Wordberfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/442,629
FILING DATE: 18-NO. 6291219-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,805A
FILING DATE: 7 JAN 1998
FILING DATE: 7 JAN 1998
FILING DATE: 7 JAN 1998
                                                               SOFTWARE: WOLDEFIECE 6.1 WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,805A
FILING DATE: 7 JAN 1998
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/JP97/00171
FILING DATE: 23 JAN 1997
APPLICATION NUMBER: JP 966
APPLICATION NUMBER: JP 966
APPLICATION NUMBER: JP 162813
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 162813
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 161813
FILING DATE: APPLICATION NUMBER: JP 161813
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WordPerfect 6.1 Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 352 KLGFKHPVIGVHVRRTDKVGTEAAF 376
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                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JAN 1996
ATTORNEY/AGENT INFORMATION:
NAME: TOFfenetti, Judith L.
REGISTRATION NUMBER: 39,048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 2356/3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
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ZIP: 20036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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544 QQEDINNNKKQEERALKQIENLQETETQLRNELEYVREELKQKRDEVKCKLD--KSEENC 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              602 NNLRKQVENKYINELQQENKALKKKGTAESKQLN--VYEIKV---NKLELELESAKQK 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 YATGGWETVFRPVSBYTCTDRSGLSTGHWSGEVKDKNVQVVELPIVDSLHPRPPYLPLAVP 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 EDLADRL--LRVHGDPAV-----WWVSQFVKYLIRPQPWLEREIEETTKKLG-F 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 ELSKILAKLERLKOQNEDLRRMAESLRIPEGPIDQGTATGR---VRVLEEQLVKAKEQIE 98
                                                                                                                                                                                     99 NYKKQARNDLGKDHBILLRRRIENGAKELWFFLQSELKKLKKLEGNELQRHADEILLDLGH
                                                                                                                                                                                                                                                                                494 YYSKEVKD-----LKTELEN-EKLKNTELTSHCNKL-SLENKELTQETSDMTLELKN
                                                                                                                                                                                                                                                                                                                                           159 HERSI------MIDLYYLSQTD----GAGEWREKEAKDLTELVQRRITYLQNPKDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356 KHPVIGVHVRRIDKVGTEAAFHPIEEYMVHVEEHFQLLERRMKVDKKRVYLATDDPSLLK
                                                              Query Match 3.8%; Score 118.5; DB 3; Length 976; Best Local Similarity 20.5%; Pred. No. 0.054; Matches 90; Conservative 74; Mismatches 164; Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9608950
GENERAL INFORMATION:
APPLICANT: OSTEOSA INC,
TITLE OF INVENTION: Ost:eoclast Growth Regulatory Factor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08950 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FP-ND 2121
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              416 EAKTKYSNYEFISDNSISW 434
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NAME: Paul C. Steinhardt
REGISTRATION NUMBER: 30,806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy
TOPOLOGY: linear
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US-09-104-324B-4
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Methods For Diagnosis And Treating Cancers,
And Methods For Identifying Pathogenic Markers In A Sample Of
No. 6232460mal Cells
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4.3%; Score 131; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY. New rot...
STATE: New York
STATE: New York
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
"...mre: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: T reci, Ozlem; Sahin, Ugur; P
TITLE OF INVENTION: Methods For Diagnosi;
TITLE OF INVENTION: And Methods For Iden
TITLE OF INVENTION: No. 6232460mal Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LiP
STREET: New York City
STATE: New York City
                                                                                                                                                                                                                         NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 2356/3
                                        FILING DATE: 22 JUL 1996
APPLICATION NUMBER: UP 162813
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: UP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: UP 10365
FILING DATE: 24 JUN 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                       192260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352 KLGFKHPVIGVHVRRTDKVGTEAAF 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
FILING DATE: 25-June-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KLGFKHPVIGVHVRRTDKVGTEAAF 25
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REFERENCE/DOCKET NUMBER: LUD 5491
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
TELEFAX: 202-429-0796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanson, No. 6232460man D.
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CLASSIFICATION: 435
PRIOR APPLICATION DATA: 08/892,702
FILING DATE: 15-July-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09104324B Patent No. 6232460
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TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TENGTH: 976 smire
                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 25 amino acids
                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-442-629-12
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SENERAL INFORMATION
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US-09-914-259-27
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                                                                                                                                                                                                                                                                                             STATE:
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                                                                                                                                                                                            509 AVYPHQPRTKEEIPMEPGDIIGVAG----NHWNGYSKGVNRKLGKTGLYPSYKVREKIET 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          509 AVYPHQPRTKEEIPMEPGDIIGVAG----NHWNGYSKGVNRKLGKTGLYPSYKVREKIET 564
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                           Query Match 3.8%; Score 116; DB 5; Length 214; Best Local Similarity 38.0%; Pred. No. 0.009; Matches 27; Conservative 12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.8%; Score 116; DB 5; Length 214; Best Local Similarity 38.0%; Pred. No. 0.009; Matches 27; Conservative 12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application PC/TUS9609127
GENERAL INFORMATION:
APPLICANT: OSTEOSA INC.
TITLE OF INVENTION: OSteoclast Growth Regulatory Factor NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Paul C. Steinhardt
REGISTRATION NUMBER: 30,806
REFERENCE/DOCKET NUMBER: FP-ND 2122
TELECOMMUNICATION INFORMATION:
TELEPRAX: (619) 535-8901
TELERAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 221, Application US/08630915A Patent No. 6309820
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LENGTH: 214 amino acids
                                                                                                                                                                                                                                                                           565 VKYPTYPEAEK 575
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rrPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-08950-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein PCT-US96-09127-2
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73 IDNPLHEAAKR 83
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 92122
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509 AVYPHOPRIKEEIPMEPGDIIGVAG----NHWNGYSKGVNRKLGKTGLYPSYKVREKIET 564
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APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFPRAN, No. 6309820h
APPLICANT: HOFPRAN, No. 6309820h
APPLICANT: FOWLKES, Dana M.
APPLICANT: FOWLKES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
ITILE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND TITLE OF INVENTION: USING SAME
NUMBER OF INVENTION: USING SAME
CORRESPONDENCE: 227
CORRESPONDENCE ADDRESS:
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APPLICANT: Hyman, Paul
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STRAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT FAPILICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 27
LENGTH: 1027
                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-:
TELECHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEFAX: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 221:
SEQUENCE CHARACTERISTICS:
LENGTH: 229 amino acids
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amino acid
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88 IDNPLHEAAKR 98
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                                                                                                                                      LGAELCEETPVNDNSS----IVVRIAPEERQKYEEEIRRLYKQLDDKDDEINQQSQL--
                                                                                                                                                                                        IMTDLYYLSOTDGAGEWREKEAKDLTELVQRRIT----YLQNPKDCSKARKLVCNINKGC
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                                                                           Gaps
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TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: DANN, DORFMAN, HERRELL AND SKILLMAN
                                                                         84; Mismatches 179; Indels 188;
                                                                                                                                                                                                                                                                                                                                                                                     R---QLENLQVECHRKMEVTGRELSSCQLLISQH------EAKIRSLTE
                                                                                                                                                                     VRVLEEQLVKAKE------QIENYKKQARNDLGKDH--EILR--
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                                            DB 4;
                                                           0.13;
                                            Score 115;
Pred. No. 0
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5599919
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APPLICANT: YEN, TIMOTHY J.
APPLICANT: RATTNER, JEROME B.
                                            3.7%;
                                           Query Match
Best Local Similarity 20.2<sup>3</sup>
Matches 114; Conservative
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COMPUTER READABLE FORM:
ORGANISM: Mus musculus
   ; ORGANISM: MU
US-09-914-259-27
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US-08-353-700-1
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86 LEEQL-VKAKEQIENYYKKQARNDLGKDHEILRRRIE----NGAKELWFFLQSELKKLKK 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 ETTKKLGFKHPVIGVHVRRTDKVGTEAAFHPIEEYMVHVEEHFQLLE---RRMKVDKKRV 404
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19.5%; Pred. No. 0.74;
.ive 90; Mismatches 206; Indels 15
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GENERAL INFORMATION:
APPLICANT: Yen, Timothy J.
APPLICANT: Rattner, Jarome B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
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                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: REED, ZANET E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-400
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 DLADRLLRVHGDPAV---
09-DEC-1994
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Matches 110; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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                                                             CLASSIFICATION:
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ORIGINAL SOURCE
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US-08-353-700-1
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us-09-971-773-23.rai

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US-09-141-206-2
; Sequence 2, Application US/09141206
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                                            740 QL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 LEGNELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGEWREKEAKDLTELVQRRITYLQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILLESQNW----RYATGGW 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETVFRPVSETCTDRSGLSTGHWSGEVKDKNVQVVELP----IVDSLHPRPPYLPLAVPE 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----WWVSQFVKYLIRPQPWLEREIE 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : : | : | : |: |: |: |: HUVLDSKSV--EVETOKTAYMELQQXA-EFSDQKHQKEIENMCLKTSQLTGQVEDLEHKL 739
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INVENTION: Expressed Kinetochore Protein, and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | | : | : : OLNDKLSKTEKESKALLSALELKKKEYEELKEEKTLFSCWKSENEKLLTO----MESEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343 LVRTTAQYDQAS---TKYTALEQKLKKLTEDLSCQRQNAESARCS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 LVRDNDHPDHSSRELSKILAKLERLKQQNEDL---RRMAESLRIPEGPIDQGTATGRVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385 LEOKIKEKEKERÉPÉBELSRŐGRSFOTLDŐBCIGMKARLTGELŐGÁKMMHNVLÓAELDKÍTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.7%; Score 115; DB 5; Length 3248;
19.5%; Pred. No. 0.74;
tive 90; Mismatches 206; Indels 158;
                                         CANDERSEE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street Suite 720
CITY: Philadelphia STATE: PA COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/16216
                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNDRAER: US 08/353,700
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
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Best Local Similarity 19.5%
Matches 110; Conservative
                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                            FILING DATE
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Sequence 63, Application US/09198452A; Sequence 63, Application US/09198452A; Sequence 63, Application US/09198452A; Sequence 63, Application:
Patent No. 6552294
GENERAL INFORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments;
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT APPLICATION NUMBER: US/09/198,452A
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 63
LENGTH: 644
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---YFGGQNAHNQIAV 510
                                  ENYKKQARNDLG--KDHEILRRRIENGAKE-----LWFFLQSELKKLKK-----L 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 RAKILPDENNSARAEQRFREVKDHWEDLN--ETVFWVKE--DGRIDIEVLTAVGGWPDRY 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---YMVHVEEHFOLLERRMKVDKKRVYLATDDPSLLKEAK 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPYLPLAVPED----LADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEREIEETTK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 LSKILAKLERLKOONEDLRRMAESLRIPEGPIDOGTA----TGRVRVLEEQLVKAKEOI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 644;
  QADFLVCTFSSQVCRVAYEIM--QTLHPDASANFHSLDDIY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.6%; Score 111.5; DB 4; Best Local Similarity 21.0%; Pred. No. 0.13; Matches 103; Conservative 73; Mismatches 190;
                                                                                                                                       : | | 1
787 FDQQPAMHASF----ANIIGEQGS 806
                                                                                                       534
                                                                                                  511 YPHQPRTKEEIPMEPGDIIGVAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-63
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31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          644 FISCSDGRTVLNKVGDEIVDRILKAHKQGWCYRVYVLL--PLL------PGFE----G 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 EQLVKAKEQI -----ENY-KKQARNDLGKDHEILRRRIENGAK-ELWFFLQSEL-- 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 -----KKLKKLEGN-ELQRHADEILLDLGHHERSIMTD--LYYLSQTDGA-GEWREK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 GINSGYSKRALMLIHPNIKVMRHPDQVTL-WAHHEKLLVVDQVVAFLGGLDLAYGRWDDL 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 EAK--DLTELVQRRITYLQNPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             469 HYRLTDLGDSSESAASQLPTPRPDSPATP------DFFHNQFFWL------ 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 LILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVKDKNVQVVELPIVDSLH-- 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   534 TTPRMPWRDVGVV-----VHGLPARDLARHFIQRWNFTKTTRAKYKIPTYPYLLPK 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 IEETTKKLGFKHP-----VIGVHVRRTDK--VGT-----EAAFHPIEE--YMVHVEEHF 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391 ------QLLERRMKVDKK----RVYLATDDPSLLKEAKTKYSNYEFISDN 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431 SISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIMQTLHPDASANF 490
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-----TYRT-LCRGEYSI----LHRLKAAMG 726
                                                                                                                                                                                                                                                                                                                                                                                        3.6%; Score 111; DB 3; Length 933;
20.5%; Pred. No. 0.25;
tive 70; Mismatches 149; Indels 180; Gaps
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Steed, Paul M.
APPLICANT: Lasala, Daniel J.
TITLE OF INVENTION: Amino Acid Sequence of Human PLD2A
Patent No. 6187559
FILE REFERENCE: 4-30148/PI/CGC1954/R
CURRENT APPLICATION NUMBER: US/09/141,206
CURRENT FILING DATE: 1998-08-27
EARLIER PILING DATE: 1997-08-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 933
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727 TAWRDYISICGLRTHGELGGHP 748
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Best Local Similarity 20.5
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Human
US-09-141-206-2
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Search completed: February 2, 2004, 08:44:36 Job time : 17.5 secs

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(without alignments)
550.686 Million cell updates/sec
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1 MRAWTGSWRWIMLILFAWGT.....YKVREKIETVKYPTYPEAEK 575
                                                                                                                                                          February 2, 2004, 08:40:23 ; Search time 217 Seconds
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/ptodata/1/pubpas/USIOA PUBCOMB.pep:
/ptodata/1/pubpas/USIOB PUBCOMB.pep:
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bcodata/1/pubpaa/US08 PUBCOMB.pep.
todata/1/pubpaa/US09A PUBCOMB.pep.
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                       Sequence:
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                                                                                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•			SUMMARIES	
Result No.	Score	Query Match	& Query Match Length DB	DB	ID	Description
7	3081	100.0	575	11	US-09-971-773-23	Sequence 23, Appl
7	3024	98.1	575	11	US-09-971-773-24	Sequence 24, Appl
m	2973	96.5	575	σ	US-09-839-136-10	Sequence 10, Appl
4	2878	93.4	575	6	US-09-839-136-2	Sequence 2, Appli
ι	2639	85.7	515	15	US-10-106-698-4658	Sequence 4658, Ap
9	431	14.0	82	σ	US-09-864-761-34720	Sequence 34720, A
7	425	13.8	81	σ	US-09-864-761-46107	Sequence 46107, A
80	133	4.3	1959	12	US-10-028-248A-36	Sequence 36, Appl
o,	132	4.3	485	12	US-10-104-047-3419	Sequence 3419, Ap
10	128	4.2	678	12	US-10-369-493-5427	Sequence 5427, Ap
11	127.5	4.1	1959	12	US-10-028-248A-106	Sequence 106, App
12	125	4.1	1961	12	US-10-028-248A-103	Seguence 103, App
13	124.5	4.0	1960	12	US-10-236-031B-62	Sequence 62, Appl
14	124.5	4.0	1960	12	US-10-028-248A-104	Sequence 104, App
15	124	4.0	405	12	US-10-094-749-3191	Sequence 3191, Ap

Sequence 273, App	Sequence 317, App	Sequence 12, Appl	Sequence 12504, A	Sequence 596, App	107,	-	Sequence 221, App	Sequence 19, Appl	43,	26(	Sequence 73, Appl	181	27,	116,	6374	79, 1	7029,	7030,		286,			22825		Sequence 3, Appli		Sequence 6, Appli	'n	Sequence 4, Appli
US-10-205-823-273	US-10-177-293-317	US-09-839-136-12	US-10-369-493-12504	US-10-117-937-596	US-10-028-248A-107	US-10-028-248A-105	US-09-879-957-221	US-09-884-001-19	US-10-369-493-43	US-10-082-830-260	US-09-893-519A-73	US-10-369-493-18106	US-10-080-608A-27	US-10-370-685-116	US-10-369-493-6374	US-10-032-189-79	US-10-369-493-7029	US-10-369-493-7030	US-10-205-823-419	US-10-097-111-286	US-10-289-762-63	US-10-369-493-21643	US-10-369-493-22825	US-10-369-493-6931	US-10-412-897-3	US-10-369-493-5702	US-10-017-216-6	US-10-017-216-5	US-10-017-216-4
15	Ŋ	σ			12		σ	10	12	15	11	12																	14
1285	1285	25	1055	976	1999	1961	229	898	1156	2383	888	896	1027	1027	2326	262	672	672	1979	586	644	880	919	1137	1441	1549	1597	1641	2055
4.0	4.0	4.0	3.9	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6
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16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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1 MRAWIGSWRWIMLILFAWGTLLFYIGGHLVRDNDHPDHSSRELSKILAKLERLKQQNEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 3081; DB 11; Length 575; 160.0%; Pred. No. 1.4e-266; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                       APPLICANT: No. US20030115614A1uo HANAI
TITLE OF INVENTION: ANTIEODY COMPOSITION-PRODUCING CELL
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 2002-08-30
PRIOR APPLICATION NUMBER: JP 2000-308526
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/268,926
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin Ver. 2.1
FIRNORM:
                                                                                                                                                                                                                                                                                      FILE REFERENCE: 249-202
CURRENT APPLICATION NUMBER: US/09/971,773
CURRENT FILING DATE: 2002-08-30
Sequence 23, Application US/09971773
Publication No. US20030115614A1
                                                                                                                  Kazuyasu NAKAMURA
Kazuhisa UCHIDA
Toyohide SHINKAWA
Naoko YAWANE
MOtoo YAWAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 160.0%;
Matches 575; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Cricetulus griseus
US-09-971-773-23
                                                                                                    Mitsuo SATOH
                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
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61 RRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIENYKKQARNDLGKDHEILRRRIE 120

1 MRAWTGSWRWIML1LFAWGTLLFYIGGHLVRDNDHPDHSSRELSKILAKLERLKQQNEDL

셤 8

9 9

Gaps

300

120 180 360 360 420 420 480 540

9 9

Gaps

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241 LILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVNDKNIQVVELPIVDSLHPR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 YSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIMQ 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLHPDASANFHSLDDIYYFGGQNAHNQIAVYPHQPRTKEBIPMEPGDIIGVAGNHWNGYS 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 PPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEREIBETTKKLGFKHPVI
                                                                                                                                                                                                                                                                                                                                                    RRMAESLRI PEGPI DOGTATGRVRVLEEQLVKAKEQI ENYKKQARNDLGKDHEI LRRRI E
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                                                                                                                                                                                                                                                                                                                                                                                                                GVHVRRTDKVGTEAAFHPIEEYMVHVEEHFQLLERRMKVDKKRVYLATDDPSLLKEAKTK
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                                                                               121 NGAKELWFFLQSELKKLKKLEGNELORHADEILLDLGHHERSIMTDLYYLSQTDGAGEWR
                                                                                                                                                              181 EKEAKDLTELVORRITYLONPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRT
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Sequence 10, Application US/09839136
Fatent No. US20020081694A1
GENERAL INPORMATION:
TITLE OF INVENTION: ALPHA 1-6 FUCOSYLTRANSFERASE
TITLE OF INVENTION: ALPHA 1-6 FUCOSYLTRANSFERASE
FILE REFERENCE: 2356-7
CURRENT APPLICATION NUMBER: US/09/839,136
CURRENT FILING DATE: 1099-11-18
FRIOR FILING DATE: 1999-11-18
FRIOR FILING DATE: 1999-10-07
FRIOR FILING DATE: 1999-10-07
FRIOR FILING DATE: 1997-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

96.5%; Score 2973; DB 9;
Best Local Similarity 95.8%; Pred. No. 6.4e-257;
Matches 551; Conservative 10; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541 KGVNRKLGKTGLYPSYKVREKIETVKYPTYPEAEK 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens US-09-839-136-10
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                                                                                       EKEAKDLTELVQRRITYLQNPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 YSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLHPDASANFHSLDDIYYFGGONAHNOIAVYPHOPRTKEEIPMEPGDIIGVAGNHWNGYS
                                                                  NGAKELWFFLQSELKKLKKLEGNELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGEWR
                                                                                                                                                   EKEAKDLTELVORRITYLONPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTORT
                                                                                                                                                                                                                                LILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVKDKNVQVVELPIVDSLHPR
                                                                                                                                                                                                                                                                                                                  PPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEREIBETTKKLGFKHPVI
                                                                                                                                                                                                                                                                                                                                       GVHVRRTDKVGTEAAFHPIEEYMVHVEEHFQLLERRMKVDKKRVYLATDDPSLLKEAKTK
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| Sequence 24, Application US/09971773
| Publication No. US20030115614A1
| GENERAL INFORMATION:
| APPLICANT: Yutaka KANDA
| APPLICANT: Yutaka KANDA
| APPLICANT: Kazuyasu NAKAMURA
| APPLICANT: Kazuyasu NAKAMURA
| APPLICANT: Kazuyasu NAKAMURA
| APPLICANT: Kazuyasu NAKAMURA
| APPLICANT: Macko YAMANE
| APPLICANT: Macko YAMANE
| APPLICANT: Mo. US20030115614Aluo HANAI
| TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL
| TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING
| TITLE REFERENCE: 249-202
| CURRENT FILING DATE: 2002-08-30
| PRIOR FILING DATE: 2000-10-06
| PRIOR FILING DATE: 2001-00-10-06
| PRIOR FILING DATE: 2001-02-16
| PRIOR FILING DATE: 2001-02-16
| RIOR FILING DATE: 2001-02-16
| SOFTWARE: Patentin Ver: 2.1
| SSOFTWARE: Patentin Ver: 2.1
| SSOFTWARE: FARENTE STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Pred. No. 1.8e-261;
9; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 97.6%;
Matches 561; Conservative
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ORGANISM: Mus musculus
US-09-971-773-24
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US-09-971-773-24
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APPLICANT: Ruben et al.

TITLE OF INVENTION: Color and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA065P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR PILING DATE: 1999-09-29
PRIOR PILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 4658
LENGTH: 515
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                                                                                                                                                                                                                                                                                                                                                     481 ALHPDASANFRSLIDIYYFGGPNAHNQIAIYPHQPRTEGEIFWEPGDIIGVAGNHWDGYP 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELWFFLOSELKKLKKLEGNELORHADEILLDLGHHERSIMTDLYYLSOTDGAGEWREKEA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 KDLTELVQRRITYLQNPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLLIE 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQNWRYATGGWETV?RPVSETCTDRSGLSTGHWSGEVXDKNVQVVELPIVDSLHPRPPYL 304
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                                                                              181 EKEAKDLTELVQRRITYLQNPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRT
                                                               LILESQNWRYATG3WETVFRPVSETCTDRSGLSTGHWSGEVKDKNVQVVELPIVDSLHPR
                                                                                                                                                                                                  GVHVRRTDKVGTENAFHPIEEYMVHVEEHFQLLERRMKVDKKRVYLATDDPSLLKEAKTK
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                                                                                                                                                                                                                                                                                                                                                                                                      KGVNRKLGKTGLYPSYKVREKIETVKYPTYPEAEK 575
                                                                                                                                                                                                                                                                                                                                                                                                                        541 KGVNRKLGRTGLYPSYKVREKIETVKYPTYPEADK 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4658, Application US/10106698; Publication No. US20030109690A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 489; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-4658
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                   TLHPDASANFHSLDDIYYFGGQNAHNQIAVYPHQPRTKEBIPMEPGDIIGVAGNHWNGYS 540
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                                                                                  EKEAKDLTELVQRRITYLQNPKDCSKAKKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRT
                                                                                                                                                                                                                     301 PPYLPLAVPEDLADRLVRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVI
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                                                               EKEAKDLTELVQRRITYLQNPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRT
                                                                                                                                                                                                  PPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEREIBETTKKLGFKHPVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION TANGET TANIGUCHI Et al.
TITLE OF INVENTION: ALPHA 1-6 FUCOSYLTRANSFERASE
FILLE REFERENCE: 2362
CURRENT APPLICATION NUMBER: US/09/839,136
CURRENT FILING DATE: 2001-04-23
PRIOR PLING DATE: 1999-11-18
PRIOR PLING DATE: 1999-11-18
PRIOR PLING DATE: 1998-01-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: EsetsEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGVNRKLGKTGLYPSYKVREKIETVKYPTYPEAEK 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 2, Application US/09839136; Patent No. US20020081694A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 92,7%
Matches 533; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Pig
US-09-839-136-2
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US-09-864-761-46107
Sequence 46107, Application US/09864761
Sequence 46107, Application US/09864761
Sequence 46107, Application US/09864761
Sequence 46107, Application US/09864761
SEREMAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hansel, David R.
APPLICANT: Chen, Wennbeng
ITILE OF INVENTION: HUAND GENE EXPRESSION NALLYSIS BY MICROARRAY
FILE REPRESSED. Acomical X.1
STILE OF INVENTION: GENE EXPRESSION NALLYSIS BY MICROARRAY
FILE REPRESSED. Acomical X.1
CURRENT FILING DATE: 2000-05-23
FRIOR FILING DATE: 2000-05-03
FRIOR PAPLICATION NUMBER: US 60/180,312
FRIOR PAPLICATION NUMBER: US 60/207,456
FRIOR FILING DATE: 2000-09-03
FRIOR PILING DATE: 2000-09-03
FRIOR FILING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                               DIN FETAL LIVER, SIGNAL = 3.5

DIN PLACENTA, SIGNAL = 4.6

DIN HBLIOO, SIGNAL = 3.6

DIN HBART, SIGNAL = 3.6

DIN LUNG, SIGNAL = 5.1

DIN BRAIN, SIGNAL = 5.1

DIN BRAIN, SIGNAL = 2.7

DIN HELA, SIGNAL = 2.7

DIN HELA, SIGNAL = 2.9

DIN HIT: QOVLZY, EVALUE 6.80e+00

NA HIT: AWOOZOGO.1, EVALUE 7.00e-44
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                                                                                                                                                                                                                    BT474, SIGNAL = 4.2
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Pred. No. 8e-31;
2; Mismatches
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00662
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                                                                                                                                   FEATURE:
CTHER INFORMATION: MAP TO AL109
OTHER INFORMATION: EXPRESSED IN
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                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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US-09-864-761-34720
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SEQ ID NO 34720
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Patent NO. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                          245 PLAVPEDLADRLVRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVIGVHV 304
                                                                                                                                                                                                                            364
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   PLAVPEDLADRILLRVHGDPAVWWVSQFVKYLIRPQPWLEREIEETTKKLGFKHPVIGVHV 364
                                                                                                                                                  RRTDKVGTEAAFHPIEEYMVHVEEHFQLLERRMKVDKKRVYLATDDPSLLKEAKTKYSNY 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DASANFHSLDDIYYFGGQNAHNQIAVYPHQPRTKEEIPMEPGDIIGVAGNHWNGYSKGVN 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   425 DASANFHSLDDIYYFGGQNAHNQIAIYAHQPRTADEIPMEPGDIIGVAGNHWDGYSKGVN 484
                                                                                                                                                                                             EFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIMQTLHP
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Annomax Sequence Listing Engine vers. 1.1
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CURRENT FILING DATE: 201-05-23

PRIOR APPLICATION NUMBER: US 60/180, 312

PRIOR APPLICATION NUMBER: US 60/180, 312

PRIOR PELLING DATE: 2000-02-04

PRIOR PELLING DATE: 2000-02-05

PRIOR PELLING DATE: 2000-02-05

PRIOR PELLING DATE: 2000-03-04

PRIOR PELLING DATE: 2000-09-03

PRIOR PELLING DATE: 2000-10-04

PRIOR PELLING DATE: 2000-10-04

PRIOR PELLING DATE: 2000-10-04

PRIOR PELLING DATE: 2001-01-30

PRIOR PELLI
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US-09-864-761-34720
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1345 LEEBERAKHNLEKQIATLH-AQVADMKKKMEDSVGCLETAEEVKRKLQKD-----LEGL 1396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 EQLVKAKEQIE-----NYKKQARNDLGKDHEILRRRIENGAKELWFFLQSELKKLKKLE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 KDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQNWRYATGGWETVFRP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 HGDPAVWWVSQFVKYLIRPQPWLEREIEETTKKLGFKHPVIGVHVRRTDKVGTEAA--FH 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 VSETCTDRSGLSTGHWSGEVKDKNV--QVVELPIVDSLHPRPPYLPLAVPEDLADRLLRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 DNDHPDHSSRELSKILAKLERLKQQ----NEDLRRMAESLRIPEGPIDQGTATGRVRVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 GNELORHADEILLELGHHERSIMTDLYYLSQTDGAGEWREKEAKDLTELVQRRITYLQNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1205 --LEQTKRVKANLEK----------AKQTL----ENER-----
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.3%; Score 133; DB 12; Length 1959; Best Local Similarity 19.1%; Pred. No. 0.041; Matches 105; Conservative 95; Mismatches 191; Indels 160;
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; Publication No. US20030236392A1
; GENERAL INFORMATION:
APPLICANT: HELLX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
FILE REFERENCE: HI-AD405
CURRENT APPLICATION NWBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
                                 PRIOR APPLICATION NUMBER: 60/272400
PRIOR FILING DATE: 2001-02-28
PRIOR PELING DATE: 2001-02-28
PRIOR PLING DATE: 2001-04-20
PRIOR PLING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/31026
PRIOR APPLICATION NUMBER: 60/311266
PRIOR PILING DATE: 2001-07-26
PRIOR PILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 211
SEQ ID NO 36
SEQ ID NO 36
                         001-01-
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ORGANISM: Homo sapiens
US-10-028-248A-36
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US-10-104-047-3419
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TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods
IITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 EVKDKNVQVVELPIVDSLHPRPPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQ 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 81;
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               PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annowax Sequence Listing Engine vers. 1.1
SEQ ID NO 46107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.8%; Score 425; DB 9; 96.3%; Pred. No. 2.7e-30; iive 2; Mismatches 1;
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APPLICATION NUMBER: PCT/US01/00661
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PRIOR FILING DATE: 2000-12-19
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Kekuda, Ramesh
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APPLICANT: Patturajan, Meera
APPLICANT: Vernet, Corine
APPLICANT: Casman, Stacie
APPLICANT: Malyankar, Uriel
APPLICANT: Shenoy, Suresh
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Zerhusen, Bryan
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Millet, Isabelle
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inger, Shlomit
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Boldog, Ferenc
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Best Local Similarity 96.3
Matches 78; Conservative
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                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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Gangolli, Esha
Miller, Charles
Conservative
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US-10-028-248A-106
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Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Goo, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 KILAKLERLK-QONEDLRRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIENYKKQ 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 LIEKLKFILLETP-PCDLQDKNIIQYQESI---LQLQELLH---LKFGVATEILLKQ--- 196
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                                                                                                                                                                                                                                                                                                       104 ARNDLGKDHEILRRRIENGAKELWFFLQSELKKLKKLEGNELORHADEI----LLDLG-- 157
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                                                                                                                                                                                                         Gaps
                                                                                                                                                                    Query Match
4.3%; Score 132; DB 12; Length 485;
Best Local Similarity 20.5%; Pred. No. 0.0063;
Matches 93; Conservative 72; Mismatches 137; Indels 152;
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 678
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096;
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3419
LENGTH: 485
                                                                                                   TYPE: PRT
CORGANISM: Homo sapiens
US-10-104-047-3419
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Best Local Similarity
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APPLICANT: Sciore, Paul APPLICANT: Millet, Isabelle APPLICANT: Millet, Isabelle APPLICANT: Rochenbergy, Mark TITLE OF INVENTION: No. US200310235882A1el Nucleic Acids and Polypeptides and Methods TITLE OF INVENTION: Thereof
                                                                                               -----FNERRAKEELQGLEIEV 302
                                                                                                                                                                                 142 GNELORHA----DEILLDLGHHERSIMTDLYYLSQTDGAGEWREKEAKDLTELVORRITYL 198
                                                                                                                                                                                                                                                                                   361 SNPLKKKAIQLQETLDTLKKQEEKLMEDMQSALTPEA---WRDKWSENWKQLNADLVVIE 417
                                                                                                                                                                                                                                                                                                                                                        199 QNPK----DCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQ------RTLILES 245
                                                                                                                                                                                                                                                                                                                                                                                          246 QNWRYATGGWETVPRPVSE-----TCTDRSGLS--TGHWSGEVKDKNVQV---- 288
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537 ISIEDMELALNEEIDNLETEEK----KIDQELAGVGKNVDSD------
                                                                                                                                                 ENYK-------KQARNDLGKDHEILRRR-IENGAKELWFFLQSELKKLK-KLE
                                             38 HSSRELSKILAKLERLKOONEDLRRMAESLRIPEGPIDOGTATGRVRVLEEQLVKAKEOI
Gaps
Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      399 VDKKRVYLATDDPSLLKEAKTKYSNYEFISDNSISWSAGLHNRYTEN 445
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Mismatches 186;
                                                                               CURRENT APPLICATION NUMBER: US/10/028,248A CURRENT FILING DATE: 2001-12-19 PRIOR APPLICATION NUMBER: 60/25619 PRIOR FILING DATE: 2000-12-19 PRIOR PLICATION NUMBER: 60/262959 PRIOR APPLICATION NUMBER: 60/262959 PRIOR FILING DATE: 2001-01-19
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; Publication No. US20030235882A1
; GENERAL INFORMATION:
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82;
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Smithson, Glennda
Zerhusen, Bryan
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Vernet, Corine
Casman, Stacie
Malyankar, Uriel
Shenoy, Suresh
Spytek, Kimberly
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Edinger, Shlomit
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laupier Jr, Raymond J
                                                                                                                        Smithson, Glennda
Zerhusen, Bryan
                                                                                                                                                                                 Colman, Steven
Tchernev, Velizar
                 Miller, Charles
Boldog, Ferenc
                                                                                                                                                                  Liu, Xiaohong
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| 110 RVKANLEKA------KQALESER-----KQALESER 1232
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1124 RASRNKAEKQKRDLGEELEALKTELEDTLDSTAAQQELRSKREQEVTVLKKTLEDEAKTH 1183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 373 EAAFHPIEEYMVHVEEHFQLLERRMKVDKKRVYLATDDPSLLKEAKTKYSNYEFISDNSI 432
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                                                                                                                                                                                                                                                                                                                                    Query Match
4.1%; Score 127.5; DB 12; Length 1959;
Best Local Similarity 19.8%; Pred. No. 0.13;
Matches 110; Conservative 79; Mismatches 177; Indels 189; Gaps
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Publication No. US20030235882A1
GENERAL INPORMATION:
APPLICANT: Shimkets, Richard
APPLICANT: Vernet, Corine
APPLICANT: Casnan, Stacie
APPLICANT: Sanan, Stacie
APPLICANT: Shenoy, Suresh
APPLICANT: Shenoy, Suresh
APPLICANT: Shenoy, Kimberly
             PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/285189
PRIOR APPLICATION NUMBER: 60/308039
PRIOR APPLICATION NUMBER: 60/308039
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 2001-09-09
NUMBER OF SEQ ID NOS: 211
SOFTWARE: PAECHLIN Ver. 2.1
SEQ ID NO 106
LENGTH: 1959
APPLICATION NUMBER: 60/272408
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US-10-028-248A-106
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US-10-028-248A-103
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APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Stone, Paul
APPLICANT: Store, Paul
APPLICANT: Store, Paul
APPLICANT: Store, Paul
APPLICANT: Millet, Isabelle
APPLICATION NUMBER: US/10/028,248A
CURRENT APPLICATION NUMBER: 60/256619
PRIOR PILING DATE: 2000-02-19
PRIOR PILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/285189
PRIOR PILING DATE: 2001-02-28
PRIOR PILING DATE: 2001-04-20
PRIOR PILING DATE: 2001-04-20
PRIOR PILING DATE: 2001-04-20
PRIOR PILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/308039
PRIOR PILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/311266
PRIOR APPLICATION NUMBER: 60/311266
PRIOR APPLICATION NUMBER: 60/311266
PRIOR PILING DATE: 2001-07-26
PRIOR PILING DATE: 2001-07-27
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19.2%; Pred. No. 0.21;
tive 94; Mismatches 191;
Si, Jingsheng
Edinger, Shlomit
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Best Local Similarity 19.2'
Matches 106; Conservative
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US-10-028-248A-103
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US-10-028-248A-104
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ORGANISM:
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1397 GL----SQRHEEKVAAYDKLEKTKTRLQQELDDLL-VDLDHQRQSACNLEKKQKK---FD 1448
                                        1345 LEEEEEEEAKHNLEKQIATLH-AQVADMKKKMEDSVGCLETAEEVKRKLQKD-----LE 1396
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438 LHNRYTE--NSLRGVILDIHFLSQADFLVCTFSSQVC-RVAYEIMQTLHPDASANFHSLD 494
                                                                                 495 DIYYFGGQNAHNQIAVYPHQPRTKEEIPMEPGDIIGVAGNHWNGYSKGVNRKLGKTGLYP 554
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95; Mismatches 191; Indels 161; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jensen, Roderick V.
APPLICANT: Gullans, Steven R.
APPLICANT: Bueno, Raphael
TITLE OF INVENTION: Diagnostic and Prognostic Tests
FILE REFERENCE: B00801/70265 (JRV/JAV)
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19.0%; Pred. No. 0.2
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CURRENT FILING DATE: 2002-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-09-05
PRIOR FILING DATE: 2001-09-05
PRIOR PPLICATION NUMBER: US 60/407,431
PRIOR PILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 102
SOCTWARE: Patentin version 3.1
LENGTH: 1960
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                                                                                                                                                                                                                                                                                                          Sequence 62, Application US/10236031B
Publication No. US20030219760A1
GENERAL INFORMATION:
APPLICANT: Gordon, Gavin J.
                                                                                                                                                                                                          1449 QLLAEEKTISAKY 1461
                                                                                                                                                                   555 SYKVREKIETVKY 567
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Best Local Similarity 19.0%
Matches 105; Conservative
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ORGANISM: Homosapiens
                                                                                                                                                                                                                                                                      RESULT 13
US-10-236-031B-62
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APPLICANT: Sciore, Paul
APPLICANT: Milet, Isabelle
APPLICANT: Rothenberg, Mark
TITLE OF INVENTION: No. US20030235882Alel Nucleic Acids and Polypeptides and Methods
TITLE OF INVENTION: Thereof
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1345 LEEEEEBAKHNLEKQIATLH-AQVADMKKKMEDSVGCLETAEEVKRKLQKD-----LEG 1396
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                                                                                                                496 IYYFGGQNAHNOIAVYPHQPRTKEEIPMEPGDIIGVAGNHWNGYSKGVNRKLGKTGLYPS 555
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19.0%; Pred. No. 0.24;
tive 95; Mismatches 191;
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PRIOR APPLICATION NUMBER: 60/25619
PRIOR APPLICATION NUMBER: 60/26619
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/272408
PRIOR FILING DATE: 2001-02-28
PRIOR PILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/308039
PRIOR PILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/311266
PRIOR FILING DATE: 2001-07-26
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Vernet, Corine
Casman, Stacie
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Shenoy, Suresh
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Edinger, Shlomit
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Best Local Similarity 19.0%
Matches 105; Conservative
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Miller, Charles
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SEQ ID NO 104
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US-10-028-248A-104
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; ORGANISM: Homo sapiens US-10-094-749-3191

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1345 LEBEBERKHNLEKQIATLH-AQVADMKKKMEDSVGCLETAEEVKRKLOKD-----LEG 1396
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                                                                                                                                                                                                                                                                            262 VSETCTDRSGLSTGHWSGEVKDKNV--QVVELPIVDSLHPRPPYLPLAVPEDLADRLLRV 319
                                                                                        142 GNELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGEWREKEAKDLTELVQRRITYLQNP 201
                                                                                                                                                                                 202 KDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQNWRYATGGWETVFRP 261
                                                                                                                                                                                                                                                                                                                                                                  320 HGDPAVWWVSQFVKYLIRPQPWLEREIEETTKKLGFKHPVIGVHVRRTDKVGTEAA--FH 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                           378 PIEEYMVHVEEHFOLLERRMKVDKKRVYLATDDPSLLKEAKTKYSNYEFISDNSISWSAG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        438 L-HNRYTENSLRGVILDIHFLSQADFLVCTFSSQVC-RVAYEIMQTLHPDASANFHSLDD 495
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88 EQLVKAKEQIE-----NYKKQARNDLGKDHEILRRRIENGAKELWFFLQSELKKLKKLE 141
                                                                                                                                                                                                                            1205 -- LEQTKRVKANLEK-----------AKQTL----ENER-----
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APPLICANT: SEKI, NACHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
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PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 3191, Application US/10094749; Publication No. US20030219741A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAWA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: MAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, JUNKO
APPLICANT: HOO, YUNKO
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OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
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42 ELSKILAKLERLKOONEDLRRMAESLRIPEGPIDOGTATGRVRVLEEQLVKAKEQIENYK 101
                                                                                                                                   116 ELSKY---KEIINROKAEIQNILDKVK----TADÓ-----LOEÓLORGKOEIENIK 159
                                                                                                                                                                              102 KQAR-----NDLGKDHEILRRRIENGAKELWFFLQSELKKLKKL--EGNELQRHADEIL 153
                                                                                                                                                                                                            216 CS----ESQLQSQCEQMKQTNINLESRLLKEEELRKEEVQTLQAELACRQTEVKALSTQV 271
                                                                                                                                                                                                                                                                                                                                                           188 ----TELVQRRIT'YLQNPKDCSK----ARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQR 239
                                                                                                                                                                                                                                                                                                                                                                                                     ------SYDKE- 314
                                                                                                                                                                                                                                                                                                                                                                                                                                              240 TLILESQNWRYATGWETVFRPVSETCTDRSGLSTGHWSGEVKDKNVQVVELPIVDSLHP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 ---VSSMGSRSSSi3G----SINARSSAEDRSPENTG-----SSVAVDNFPQVDK--- 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 RPPYLPLAVPEDLADRILLRVHG--DPAVWWVSQFVKYLIRPQPWLEREIEETTKKLGFKH
                                           54; Mismatches 109; Indels 118; Gaps
Length 405;
                                                                                                                                                                                                                                                                                                                                                                                         272 EELKDELVTORRKHASSIKDLTKOLOQARRKLDQVESG----
                                                                                                                                                                                                                                                                 154 LDLGHHERSIMTDLYYLSQTD-----GAGEWREKEAKDL
Query Match 4.0%; Score 124; DB 1; Best Local Similarity 21.9%; Pred. No. 0.025; Matches 79; Conservative 54; Mismatches 10
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 2, 2004, 08:39:43; Search time 17 Seconds (without alignments) 3252.764 Million cell updates/sec Run on:

Title: Perfect score:

US-09-971-773-23 3081 1 MRAWTGSWRWIMLILFAWGT......YKVREKIETVKYPTYPEAEK 575 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	glycoprotein 6-alp		sp8 protein - fiss	myosin-like coiled	protein C18H9.8 [i	myosin heavy chain			synaptonemal compl	hypothetical prote		364K Golgi complex	conserved hypothet	adaptor protein in		probable heat shoc	restin - human	•	당	glycoprotein A - m	synaptonemal compl	chromosome assembl	kinesin heavy chai	myosin heavy chain		hypothetical TPR/T	microtubule-vesicl	heavy cha	myosin II heavy ch
SUMMARIES	Ω	JC5432	T32154	T43527	T50073	H88187	A33977	S28061	A61231	148176	H86250	T08621	JC5837	A70387	T09194	B43402	D96796	S22695	846327	S21801	JE0120	S49461	B70356	S37711	A59252	T29140	S23741	A43336	360	S61477
	DB		~	~	7	~	٦	~	н	~	~	~	~	7	N	-	N	~	N	н	~	~	~	7	7	~	4	N	Н	7
	Length	575	818	1173	1727	678	1959	946	1961	845	1025	2442	3187	978	1270	2007	1871	1427	581	1999	1282	993	1156	1027	1976	2326	503	1392	2017	2057
	% Query Match	96.9	32.3	4.3	4.3	4.2	4.1	4.1	4.1	4.0	4.0			3.9	٠				٠		•				•	•	3.7	•	•	•
	Score	2984	995	133	133	128	127.5	127	125	124.5	124	124	121.5	120.5	119.5	119.5	119	118.5	118	118	117.5	116	116	115	115	115	114.5	114.5	114.5	114.5
	Result No.	1	7	٣	4	Ŋ	9	7	60	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote	hypothetical prote	myosin heavy chain	hypothetical prote	hypothetical prote	myosin heavy chain	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	citron - mouse				
382905	T22507	IX0178	AE1568	C83696	S24348	T04501	E86496	F81543	F75103	B72765	T33338	T51505	T19414	T21809	S68420
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2 I	2	-1	7	~	7	7	7	7	7	7	7	7	7	7	~
7	. 672 2 7	-	465 2	532 2	955 2	398 2	642 2	642 2	880 2	919 2	1023 2	853 2	1137 2	1549 2	1597 2
7	7	-	3.6 465 2	3.6 532 2	3.6 955 2	3.6 398 2	3.6 642 2	3.6 642 2	3.6 880 2	3.6 919 2	3.6 1023 2	3.6 853 2	3.6 1137 2	3.6 1549 2	3.6 1597 2
3.7 435 2	7	3.7 1938 1	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6

# ALIGNMENTS

RESULT 1 JC5432 glycoproteir N;Alternate	RESULT 1 JCS432 glycoprotein 6-alpha-L-fucosyltransferase (BC 2.4.1.68) precursor - human N;Alternate names: alpha 1-6 FucT; GDP-L-fucose:N-acetyl-beta-D-glucosaminyl:6-alpha-L-f
C;Species: 1 C;Date: 03-1	C.Species: Homo sapiens (man) C.Sate: 03.Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Jun-2000
C, Accession R, Yanagidan:	C.Accession: UC3426; FC4322 Ysnangidani, S., Uozumi, N.; Ihara, Y.; Miyoshi, E.; Yamaguchi, N.; Taniguchi, N.
A;Title: Pu:	o. brochem. 11, 22, 23, 13, 13, 13, 13, 13, 13, 13, 13, 13, 1
A; Accession: JC5432 A; Molecule type: mRNA	: JC5432 Lype: mRNA
A;Residues: A;Cross-refe	A;Residues: 1-575 <yan1> A;Cross-references: DDbJ:D89289; NID:g2055306; PIDN:BAA19764.1; PID:g2055307</yan1>
A; Molecule type: pr	A.Accession: PC4322 A.Molecule type: protein
C; Comment:	
A;Generics: A;Gene: GDB:FUT8 A;Cross-referenc	A.Gross.rUT8 A.Gross.references: GDB:9786294; OMIM:602589
A, Map posit: C, Superfami	A;Map position: 14q23-14q23 C;Superfamily: human glycoprotein 6-alpha-L-fucosyltransferase
C; Keywords: F;1-22/Doma: F;23-575/Pro	C;Keywords: glycosyltransferase; hexosyltransferase F;1-22/Domain: signal sequence #status predicted <sig> F;23-575/Product: glycoprotein 6-alpha-L-fucosyltransferase #status predicted <mat></mat></sig>
Query Mato Best Loca Matches	Query Match Best Local Similarity 96.2%; Pred. No. 2.2e-186; Matches 553; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
ò	1 MRAWIGSWRWIMLILFAWGTLLFYIGGHLVRDNDHPDHSSRELSKILAKLERLKQQNEDL 60
Ωp	1 MRPWTGSWRWIMLILFAWGTLLFYIGGHLVRDNDHPDHSSRELSKILAKLERLKQQNEDL 60
λō	61 RRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIENYKKQARNDLGKDHEILRRRIE 120
Op QD	61 RRMAESLRIPEGPIDQGPAIGRVRVLEEQLVKAKEQIENYKKQTRNGLGKDHEILRRRIE 120
Qy 1:	121 NGAKELWFFLOSELKKLKKLEGNELORHADEILLDLGHHERSIMTDLYYLSQTDGAGEWR 180
Db 13	121 NGAKELWFFLQSELKKLKNLEGNELQRHADEFLLDLGHHERSIMTDLYYLSQTDGAGDWR 180
07 11	181 EKEAKDLIELVQRRITYLQNPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRT 240
Db 1	181 EKEAKDLTELVQRRITYLQNPKDCSKAKKLVCNINKGCGYGCQLHHVVYCFWIAYGTQRT 240
Qy 2,	241 LILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVKDKNVQVVELPIVDSLHPR 300
Db 2,	241 LILESQNWRYATGGWETVFRPVSETCTDRSGISTGHWSGEVKDKNVQVVELPIVDSLHPR 300

QY 399 VDKKRVYLATDDPSLLKEAKTKYSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLS 458 :: :: :   ::		519 BEIPMEPGDIIGVAGNHANGYSKGVNRKLGKTGLYPSYKVR 559	TINE 3	14352/ 19552/1 - fission yeast (Schizosaccharomyces pombe) (fragment) C,Species: Schizosaccharomyces pombe C,Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 04-Feb-2000	Ridimens, M.; Goday, C. submitted to the EMBL Data Library, June 1997 A.Description: Schizosaccharomyces pombe myosin-like. A;Reference number: 222545 A;Accession: T43527 A;Status: translated from GB/EMBL/DDBJ	A;Molecule type: mRNA A;Residues: 1-1173 <jim> A;Cross-references: EMBL:AF010473; PIDN:AAB65416.1 A;Experimental source: strain 972h(-) C;Genetics:</jim>	A;Gene: Sp8 Query Match Query Match Best Local Similarity 21.2%; Pred. No. 1.3; Matches 110; Conservative 74; Mismatches 226; Indels 108; Gaps 20;	QY 34 DHPDHSSRELSKILAKLERLKQQNEDLRRMAESLRIPEGPIDQGTATGRVRVLEEQLVKA 93 :		72 7	186 DIFELVQRATITYLQRANKAU-CANANKAU-CUINNAC-GIGCQARHAVYICFRATAGGIGCATAGGIGCAGARAVICFRATAGGIGCAGARAVICFRATAGGIGCAGARAVICAGARAVIC	246 QNWKIALIGGWEIVERFVSELLINGSGESIGEMSGEVOLNVQVELFINGSELLINGSGESIGEN SELLEN VERFIGERINGSGESIGEN VERFIGERINGSGESIGEN VERFIGER VERFIGERINGSGESIGEN VERFIGER VE	306 LAVPEDLADRLILR   : 879 TATTQ	366 KIDKY	LODOVKALQETVVSSEEAESASVHADTKDLENLKKTEEMLSVTFQVIFNESISDFSTSTA	Oy 461 DFLVCTFSSQVCRVAYEIMQTLHPDASANNHSLDD1 496
Oy 301 PPYLPLAVPEDLADRLLRVHGDPAVWWVSQPVKYLIRPQPWLEREIEETTKKLGFKHPVI 360 	OY 361 GVHVRRIDKVGTEAAFHPIEEYMVHVEEHFQLLERRMKVDKRVYLATDDPSLLKEAKTK 420	OY 421 YSNYBFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYBINQ 480 	QY 481 TLHPDASANFHSLDDIYYFGGQNAHNQIAVYPHQPRTKEEIPMEBGDIIGVAGNHWNGYS 540	OY 541 KGVNRKLGKTGLYDSYKVREKIETVKYPTYPEAEK 575 	RESULT 2 T32154 hypothetical protein C10F3.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 29-Oct-1999 #sequence revision 29-Oct-1999	C;Accession: T32154 R;Davidson, S.; Wohldmann, P. submitted to the EMBL Data Library, September 1997 A;Description: The sequence of C. elegans cosmid C10F3. A;Reference number: Z21127	A.Accession: T32154 A.Status: preliminary; translated from GB/EMBL/DDBJ A.Molecule type: DNA A.Residues: 1-818 < DAV> A.Cross-references: EMBL:AF022968; PIDN:AAB69888.1; GSPDB:GN00023; CESP:C10F3.6	· .	A;Introns: 30/1; 72/2; 235/2; 258/3; 285/2; 315/3; 457/3; 491/1; 544/3; 556/1; 626/1; 64 Query Match Best Local Similarity 36.7%; Pred. No. 7.4e-57; Matches 213; Conservative 116; Mismatches 188; Indels 64; Gaps 11;	RELSKILAKLERLKQQNEDLRR 6	QY 63 MAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIENYKKQARND 107 :	Qy 108LGK-DHEILRRRIENGAKELWFFLQSELKKLKKLEGNELQRHADEILLDLGHHERSIM 164	QY 165 TDLYYLSQTDGAGEWREKEAKDLTELVQRRITYLQNPKDCSKARKLVCNINKGCGYGCQL 224    :           :   :	QY 225 HHVVYCFMIAYGTQRTLILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGE 280	Qy 281 VKDKGVQVVELPIVDSLHPRPPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQP 340 :	Qy 341 WLEREIEETTKKLGF-KHPVIGVHVRRTDKVGTEAAFHPIEEYMVHVEEHPQLLERRM-K 398 : ::::   :

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A;cross-references: GB:X17589
A;Note: this translation is not annotated in GenBank entry GGMHCFWHA, release 114
R;Hodge, T.P.; Cross, R.; Kendrick-Jones, J.
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A;Residues: 716-1008 <KAT>
                                           A; Molecule type: DNA
* Pacidues: 1-678 <STO>
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                                  A;Status: preliminary
A; Accession: H88187
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A, Map position:
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: H8B187
R;anorymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C elegans/ and www.sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                          (Schizosaccharomyces pomb
                                                                                                                                                                                                                                                                                                                                                                                                                        GSPDB:GN00066; SPDB:SPAC1486.04c
                                                                                 myosin-like coiled-coil protein sp8 [imported] - fission yeast (Schizosaccharomy c) myosin-like coiled-coil protein sp8 [imported] - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe C;Species: Og-Jun-2000 #text_change Og-Jun-2000 C;Accession: T50073 R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D. R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D. A;Accession: T50073 A;A
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myosin heavy chain, nonmuscle - chicken
N;Contains: myosin ATPase (EC 3.6.4.1)
(S.Species: Gallue gallue (chicken)
C;Species: Gallue gallue (chicken)
C;Accession: A33977; S06116; A43422
C;Accession: A33977; S06116; A43422
C;Accession: A33977; Conti, M.A.; Kawamoto, S.; Preston, Y.A.; Brill, D.A.; Adelstein, R.S. Proc. Natl. Acad. Sci. US.A. 86, 7726-7730, 1989
A;Title: Cloning of the CDNA encoding the myosin heavy chain of a vertebrate cellular my A;Reference number: A33977; MuID:90046668; PMID:2813355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     are differentially expressed in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :: | | : | | :: | 303 EEQKKIANEAVTHAMDPQMKEKYEDLKSEAKLIRERVVEMEAKN--EDLDDRISKYEIEIR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNELORHA----DEILLDLGHHERSIMTDLYYLSQTDGAGEWREKEAKDLTELVQRRITYL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ONWRYATGGWETVFRPVSE------288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              629
                                                                                                                                                                                                                                                                                                                                                                                                                  --FNERRAKEELOGLEIEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QNPK----DCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQ------RTLILES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                418 KOHKTVKDOISLASEELHEYDSOGEAQIMAHHTKYLDLLSKSTMLDDTTENYPQQIVIYQ
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                                                                                                                                                                                                                                                                                                                                                38 HSSRELSKILAKLERLKOONEDLRRMAESLRIPEGPIDOGTATGRVRVLEEQLVKAKEQI
                                                                                                                                                                                                                                                                                  Gaps
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A;Residues: 1-1959 <8HO>
A;Cross-references: GB:M26510; NID:g212382; PIDN:AAA48974.1; PID:g212383
A;Cross-references: GB:M26510; NID:g212382; PIDN:AAA48974.1; PID:g212383
A;Txteuragawa, Y.; Yanagisawi, M.; Inoue, A.; Masaki, T.

Bur. J: Biochem. 184, 611-616, 1989
A;Title: Two distinct nonmuscle myosin-heavy-chain mRNAs are differential
A;Residues: 1-678 <STO>
A;Cross-references: GB:chr_XI; PID:g722387; GSPDB:GN00020; CESP:C18H9.8
                                                                                                                                                                                                                                                                                  Indels 108;
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                                                                                                                                                                                                             Length
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                                                                                                                                                                                                             7
                                                                                                                                                                                                         4.2%; Score 128; DB 19.5%; Pred. No. 1.4; tive 82; Mismatches
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C;Accession: S28061
K;Meuwissen, R.L.J.; Offenberg, H.H.; Dietrich, A.J.J.; Riesewijk, A.; van Iersel, M.; H
EMBO J. 11, S011-5100, 1992
A;Title: A coiled-coil related protein specific for synapsed regions of meiotic prophase:
A;Reference number: S28061; MUID:93099884; PMID:1464329
A;Accession: S28061
A;Accession: S28061
A;Molecule type: mRNA
A;Residues: 1-946 <MEU>
A;Cross-references: EMBL:X67805; NID:g57212; PIDN:CAA48006.1; PID:g57213
C;Genetics:
A;Gene: SCP1
C;Keywords: DNA binding
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J. Cell Biol. 118, 1085-1095, 1992

A; Title: Role of the COCH-terminal nonhelical tailpiece in the assembly of a vertebrate A; Reference number: A43422; MUID:92381096; PMID:1512291
A; Recession: A43422
A; Status: nucleic acid sequence not shown; not compared with conceptual translation A; Molecule type: mRNA
A; Residues: 1900-1959 «HOD»
A; Experimental source: brush border
A; Note: sequence extracted from NCBID backbone (NCBIP:111947)
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleotid F; 847-64/Domain: myosin motor domain homology cMMOT>
F; 174-181/Region: nucleotide-binding motif A (P-loop)
F; 552-565/Region: actin binding #status predicted
F; 837-1277/Region: coiled coil #status predicted
F; 837-1277/Region: S2
F; 1278-1955/Region: 1ight meromyosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1233 VKVÍLQGKGDAEHKRKKVDAQLQELQVKFTEGER------VKTELAERVNKÍQVELDNV 1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTORY-----EEKIAAYDKLEKTKTRLQQELDD-IAVDLDHQRQTVSNLEKKQKK--- 1445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 VWWVSQ----FVKYLIRPQPWLEREI------ETTTKKLGFKHPVIGVHVRRTDKVGT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1124 RASRNKAEKQKRDLGEBLEALKTBLEDTLDSTAAQQELRSKREQEVTVLKKTLEDBAKTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----QEMRQKHSQAIEELAEQ------LEQTK
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EDEKNALKEQLEEBEBEAKRNLEKQISVLQQQAV------EARKKMD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 ELSKILAKLE-RLKQQNEDLRRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 ADEILLDLGHHERSIMTDLYYLSQTDGAGEWREKEAKDLTELVQRRITYLQNPKDCSKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQNWRYATGGWETVFRPVSETCTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1959;
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tive 79; Mismatches 177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.1%; Score 127.5;
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1937-1959/Domain: carboxyl-terminal <CBT>
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Best Local Similarity 19.8
Matches 110; Conservative
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                                                                                                                                                                                                                                          HAD-----EILLDLGHHERSIMTDLYYL--SQTDGAGEWREKEAKDLTELVQRRITYLQ 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K-----KQARNDLGKD------HEILRRRIENGAKELWFFLQSELKKLKCHEGNELQR
                                                                                                                                                                                                                                                                                                                       200 NPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQNWRYATGGWETVF
                                                                                                                                                                                                                                                                                                                                                             265 EKKDHLTS-------ELEDIKMSMQRSMSTQKTL---EEDLQIAT---KTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                          304 QLTEEKEAQMEELNKAKTTHSLVVTELKATTCTLEELLRTEQQRLENNEDQLKLITMELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --SGEVKD----KNVQVVELPIVDSLHPRPPYLPLAVPEDLADRLLRVHG-DPAVMWVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 FVKYLI--RPQPWLEREIEEŢTKKLGFKHPVIGVHVRRTDKVGTEAAFHPIEEYMVHVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HFQLLERRMKVDKKRVYLATDDPSLLKEAKTKYSNYEFISDNSISWSAGLHNRYTENSLR
                                                                         ELSKILAKLERLKQQNEDLRRMAESLRIPEGPIDQGTATGR-VRVLEEQLVKAKEQIENY
                                                                                                                   ------IKENNATRHWCNLLKETCARSAEKTSKY
                                                                                                                                                                                                                                                                                 210 EVNNKENQVSLLLLIQSTEKENKMKDLTFLLEESRDKANQLEEK-----TKLQDENLKELN
                                       Gaps
                                     Mismatches 188; Indels 138;
Length
                                                                                                                                                                                                                                                                                                                                                                                                         ------TCTDRSGLSTGHW-
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7
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Score 127; DB Pred. No. 2.5;
                                     86;
4.1%;
20.3%;
                                                                                                    | |: || |:|||
|104 ENEKVSLKLEEEIQENKDL
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         260 RPVSE-----
                  Similarity
                Local Simi
                                                                               42
  Query Match
                                                                                                                                                              101
                                                                                                                                                                                                                                            148
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                                     Matches
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genes located on differe D.; Adelstein, myosin heavy chain nonmuscle form A - human NiAlternate names: cellular myosin heavy chain; myosin type 9; NWMHC-A NiContains: myosin APPase (EC 3.6.4.1) Cispecies: Homo sapiens (man) Cispecies: Man, Mang, Mang, Mishelferie, O.W.; Kawamoto, S.; Yamakawa, K.; Gdula, D. Risimons, M.; Wang, M.; Morbride, O.W.; Kawamoto, S.; Yamakawa, K.; Gdula, D. A; Title: Human nonmuscle myosin heavy chains are encoded by two genes locate A; Reference number: A61231; MUID:91316803; PMID:1860190

A; Accession: A6123

A;Molecule type: mRNA A;Residues: 1-715 <SIM> A;Cross-references: GB:M69180; NID:g189029; PIDN:AAA61765.1; PID:g189030 A;Cross-references: GB:M69180; NID:g189029; PIDN:AAA61765.1; PID:g189030 R;Saez, C.G.; Myers, D.C.; Shows, T.B.; Leinwand, L.A. Proc. Natl. Acad. Sci. U.S.A. 87, 1164-1168, 1990 A;Title: Human nonmuscle myosin heavy chain mRNA: generation of diversity through altern

SCP1 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 08-Oct-1999

RESULT 7

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R. Dobson, M.J.; Pearlman, R.E.; Karaiskakis, A.; Spyropoulos, B.; Moens, P.B. J. Cell Sci. 107, 2749-2760, 1994
A. Fitle: Synaptonemal complex proteins: occurrence, epitope mapping and chromosome disjuminement unmber: 148176; MUID:95181577; PMID:786343
A. Reference number: 148176
                                                                                                                                                                      347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204
               LHNRYTE--NSLAGVILDIHFLSQADFLVCTFSSQVC-RVAYEIMQTLHPDASANFHSLD 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---SKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQ--NWRYATGGWETVF 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETTKKLGFKHPVI(3VHVRRTDKVGTEAAFHPIEEYMVHVEEHFQLLERRMKV---DKKRV 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERDSELGL-----CKNREQEQLSVKTA---LETELSNIRNELVSLKKOLEIEREEKEKL 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synaptonemal complex protein - golden hamster (fragment)
C;Species: Mesocricetus aunatus (golden hamster)
C;Date: 02-Jul-1996 #sequerce_revision 02-Jul-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 YKKQARNDLGKDHEILRRRIENGAKELWFFLQSELKKLK-----KLEGNELQRHADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELSKILAKLERLKQQNEDLRRMAESLRIPEGPID--QGTATGRVRVLEEQLVKAKEQIEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 ELKKILAEDOKLLDEKKOVBKLAEBLOGKEOBLTLLLOTREKEVHDLEEOLLVTKISDON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 ILLDLGHHERSIMT----DLYYLSQTDGAGEWREKEAKDLTELVQRRITYLQNPKDC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     390 MALELKKYQEDITNSKKQEERMLKQIENLEE-KETHLRDELESVRKEFIQQGNEVKCKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         495 DIYYFGGONAHNJIAVYPHQPRIKEEIPMEPGDIIGVAGNHWNGYSKGVNRKLGKTGLYP
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C;Genetics:
A;Gene: syn1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 845;
                                                                           1345 LEEEEEEAKHNLIKQIATLH-AQVADMKKKMEDSVGCLETAEEVKRKLQKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 4.0%; Score 124.5; DB 2; Similarity 18.8%; Pred. No. 3.1; 22; Conservative 84; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 RPVSETCTDRSGLSTGHWSGEVKDKNVQVVEL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                         QLLAEEKTISAKY 1461
                                                                                                                                                                                                                                                              555 SYKVREKIETVK<sub>X</sub> 567
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Best Local Simi
Matches 82;
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A,Reference number: A34876; MUID:90138958; PMID:1967836
A,ACCession: A34876
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A,ACCESSION: A3587
A,ACCESSION: A3574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LQVELDNVTGLLS------QSDSKSSKLTKDFS 1304
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4.1%; Score 125; DB 1; Length 1961;
Best Local Similarity 19.2%; Pred. No. 8.9;
Matches 106; —Conservative 94; Mismatches 191; Indels 162;
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: T08621
R;Mack, G.J.; Rees, J.; Sandblom, O.; Balczon, R.; Fritzler, M.J.; Rattner, J.B.
Arthritis Rheum. 41, 551-558, 1998
A;Title: Autoantibodies to a group of centrosomal proteins in human autoimmune sera a A;Reference number: Z16462; MUID:98165428; PMID:9506584
A;Accession: T08621
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2442 cmAc>
A;Cross-references: EMBL:AF022655; NID:92832236; PIDN:AAC06349:1; PID:92832237
A;Experimental source: cell line HeLa
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                  Riveologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hudhes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Joenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Veneer, J.C.; Davis, R.W.
A;Tille: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Retus: preliminary
A;Molecule type: DNA
A;Retus: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AE005172; NID:g4835785; PIDN:AAD30251.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EETTKKLGFK---HPVIGVHVRRTDKVGTEAAFHPIEEYMVHVEEH 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|:| | :: | |: :| |: :| 362 SGNW-WFAEVVVPGGALVIDWVFADGPPKGAFLYDNNGYQDFHALVPQKLPEELYWLEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 -----PRPPYL-PLAVPEDLADRLLRVHG----DPAVW--WVSQFVKYLIRPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                747 AMTFADKATTVSPTYAKEVAGNSVISAHLYKFHGIINGIDPDIWDPYNDNFI----PVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             802 YTSENVVEGKRAAKEELQNRLGLKSADFPVVGIITRLTHQKG------IHLIKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 TGSWRWIMLILFAWGTLLF-YI-----GGHLVRDNDHPDHSSRELSKILAKLERLKOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEDLRRMAESLRI PEGPI -----DQGTATGRVRVLEEQLVKAKEQI ENYKKQARNDLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 KDHEIL---RRRIENGAKELWF--FLOSELKKLKKLEGNELQRHADE-----ILLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             592 VGGLGDVVTSLSRAVQELNHNVDIVFPKYDCIKHNFVKDLQFNRSYHWGGTEIKVWHGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----INKGCGYGCQ-----LHHVVYCFMIAYGTQRTLILESQNWRYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 TGGWETVFRPVSETCTDRSGLSTGHWS--GEVKDKNVQVVELPIVDSLH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----DKKRVYLATDDPSLLKEAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                      240;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 1025;
                                                                                                                                                                                                                                                                                                                                                                                                            4.0%; Score 124; DB 2; Length 102 ilarity 18.6%; Pred. No. 4.3; Conservative 79; Mismatches 184; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----DLTELVORRITYLON----PK-DCSK---ARKLVCN-
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Best Local Similarity
Matches 115; Conserv
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centrosome associated protein CEP250 - human C; Species: Homo sapiens (man)

RESULT 11

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A,Molecule type: mRNA

A,Residues: 1-3187 < TOKS.

A,Residues: 1-3187 < TOKS.

A,Cross-references: DDBJ:D25543; NID:G516825; PIDN:BAA05026.1; PID:G516826

C,Comment: This protein plays a role in the formation and maintenance of the characteris

C,Superfamily: giantin

E,Superfamily: giantin

E,49-549, 624-1176, 1238-1707, 1763-3114/Domain: coiled-coil leucine zipper #status predict

P,3165-3187/Domain: membrane anchor #status predicted <MAD>
                                                                                                                                                                                                                           1038 RETOEYNRIQKELEREKASLTLSLMEKEQRLLVLQEADSIRQQELSALRQDMQEAQGEQK 1097
                                                                                                                                                                                                                                                                                                                                                                                                                   --KQ 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1148 KAAQLH-----LRLRSTESQLEALAAEQQPGNQAQAQLASLYSALQQALGSVCESRP 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1202 ELSGGGDSAPSVWGLEPDQNGAR-----SLFKRGPLLTALSAEAVASALLKLHQD-- 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444
                                                                                                                                           985
                                                                                                                                                                                        137
                                                                                                                                                                                                                                                                                       138 KKLE-----GNELORHADEILLDLGHHERSIMT-------DLYYLSQ--TDGAGEWR 180
                                                                                                                          271 GLSTGH-----WSGEVKDKNVQVVELPIVDSLHPRPPYLPLAVPEDLADRLLRVHGDPA
                                                                                            43 LSKILAKLERLKQQNEDLRRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIENYKK
                                                                                                                                                                                                                                                                                                                                                                                   E-----KEAKDLTELVQRRITYLQNPKDCSKARKLVCNINKGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 VWWVSQFVKYLIRPQPWLEREIEETTKKLGFKHPVIGVHVRRIDKVGTEAAFHPIEEYMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HVEEHFOLLERRMKVDKKRVYLATDDPSLLKEAKTKYSNYEFISDNSISWSAGLHNRYTE
                                                                                                                                                                                          QARNDLG------KDHEILRRRIENGAKELWFFLQSEL-------KKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 YGCQLHHVVYCFMIAYGTQ----RTLILESQNWRYATGG-----WETVFRPVSETCTDRS
4.0%; Score 124; DB 2; Length 2442;
19.6%; Pred. No. 14;
Attive 76; Mismatches 139; Indels 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SQNQEEKSKWEG----
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                                                    Conservative
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                           Similarity
  Query Match
Best Local Simi
Matches 96;
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Query Match 3.9%; Score 121.5; DB 2; Length 3187; Best Local Similarity 19.0%; Pred. No. 29; Matches 108; Conservative 76; Mismatches 177; Indels 207; Gaps 24;	234 BEKUSLEKELSQVVTKLKELENLEREVEKLKERKLEFSKKVAPTVFIARKIEELDRALIEL 73 PIDQGTATGRVRVLEEQLVKAKEQIENYKKQARNDLGKDH 2
OY 27 GHLVRDNDHPDHSSRELSKILAKLERLKQONEDLRRMAESLRIPEGPIDQGTATGRVRVL 86	
QY 87 EEQLVKAKEQIENYKKQARNDLGKDHEILRRRIENGAKELWFFLQSELKKLKKLEGNELQ 146   ::	354 BLSQLSSSLKEKERNYEQAKQEFEDLSERVEKG-KKLVAETTEKLEKLKELFSBEEYTSL 144ELQRHADELLDLGHHERSIMTDLYYLSQTDGAGEWREKEAKDLTELVQRRI
Qy 147 RHADBILLDLGHHERSIMTDLYYLSQTDGAGEWREKEAKDLTELVQR 193   :     :     :   :     :     138   EKLDALHREKAHVEDTLAEIQVSLTRKDKDMKELQQSLDSTLAQLAAFTK 2128	413 KWKERLLVELORKLIGELKEKEGQLENLIQKYFERKKVHEKVLNEL 196 TYLONPKDCSKARKLVCNINKGCGYGCQLH-HVVYCFMIAYGTQRTLILESQN  :
QY         194 RITYLONPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQNWRYATG 253           Db         2129 SMSSLQDDRDRVIDEAKKWEQRFG 2152	458 KELERELKEKER
Qy         254 GWETVERPVSETCTDRSGLSTGHWSGEVKDKNVQVVELPIVDSLHPRPPYLPLAVP 309           Db         2153 DAIQTKEEEVRLKEENCTALKDQLRQMTIHM 2183	DD 501 341  QY 295 DSLHPRPPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLER 344
Qy 310 EDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEREIEFTTKKLGFKHPVIGVHVRRTDK 369	345EIEETTKKLGFKHPVIGVHVRRTDKVGTEAAFHPIEEYMVH
QY 370 VGTEAAFHPIEEYMVHVEEHFQLLERRMKVDKRRVYLATDDPSLLKEAKTKYSNYEFISD 429  1	602 HAAQTELELLÄEKIREKSKLUVKEFKELIKVEKLEDTE 386 VEEHF-QLLERRHKVDKKRVYLATDDPSLLKEAKTK ::
OY 430 NSISWBAGLHN-RYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIMQTLHP 484	Db 662 LRKHFEELSSRKSFLEGELSAINEJEEERKEK 697 RESHIF 14
485 DASANFHSLDDIYYFGQNAHNQIAVYP-HQPRTKEEI PMEPGDIIGVAGNHWNGYSKGV 543 2312 BINVKEQKIISLLSSKEEEIQVAIARIAQUSKBIKEISNLLQQEE 2357	109194. adaptor protein intersectin - African clawed frog c;ppcies: Xenopus laevis (African clawed frog) C;Date: 11-Jun-1999 #sequence revision 11-Jun-1999 #text_change 21-Jul-2000
NRKLGKTGLYPSYKVREKIETVK 566     : ::   :    :    :    :    :    :	C; Accession: T09194 R; Yamabhai, M.; Hoffnan, N.G.; Hardison, N.L.; McPherson, P.S.; Castagnoli, L.; Cesareni J. Biol. Chem. 273, 31401-31407, 1998 A; Title: Intersectin, a novel adaptor protein with two eps15 homology and five src homol A; Reference number: 21605; MUTD:99030416; PMID:9813051
RESULT 13 A70387 A70387 Conserved hypothetical protein aq_1006 - Aquifex aeolicus C;Species: Aquifex aeolicus C;Species: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 02-Feb-2001 C;Accesion: A70387 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov	A; Accession: T09194 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Mesidues: 1-1270 < YAM> A; Residues: 1-1270 < YAM> A; Cross-references: EMBL: AF032118; NID: g2642624; PIDN: AAC73068.1; PID: g2642625 A; Experimental source: cell type cocyte C; Function: A; Description: involved in endocytosis
Aquifex aeolicus.	C;Keywords: endocytosis Query Match Best Local Similarity 20.6%; Pred. No. 11; Matches 121; Conservative 82; Mismatches 174; Indels 211; Gaps 33;
Status: preliminary; nucleic Molecule type: DNA Mosiques: 1-978 <aqf> Cross-references: GB:AE00071</aqf>	Qy 41 RELSKILAKLERLKQQNEDLRRMAESLRIPEGPIDQGTATGRVRVLEEGLVKAKEQIENY 100   :     :     :     :     :     :     :   Db 375 RKEQERLAQLERAEDERKEREQDGERKRQQDLEKQLEKQRE-LERQ 420
A;Experimental source: strain VF5 C;Genetics: aq_1006 C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032	QY 101 KKQARNDLGKDHEILRRRIENGAKELWFFLQSELKKLKKLEGNELQRHADEILLDLGHHE 160 :::
Query Match 3.9%; Score 120.5; DB 2; Length 978; Best Local Similarity 18.2%; Pred. No. 6.9; Matches 94; Conservative 80; Mismatches 161; Indels 181; Gaps 18;	Qy 161 RSIMTDLYYLSQTDGAGEWREKEAKDLTELVQRRITYLQNPKDCSKARKLVC 212  Qy 161 RSIMTDLYYLSQTDGAGEWREKEAKDLTELVQRRITYLQNPKDCSKARKLVC 212  Db 457NQRNREQEDIVVLKAKKKTLEFELBALNDKKHQLEGKLQDIRC 499
Qy 34 DHPDHSSRELSKILAKLERLKQQNEDLRRMAESLRIPEG 72 :                 :::         :::	Qy 213 NINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQNWRYATGGWETVFRPVSETCTDRSGL 272 

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-----YYLSQTDGA-GEWREKEAKD 186
40 SRELSKILAKLERLKQQNEDLRRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIEN 99
                                                                                                                - KDHEILRRRIENGAKELWFFLQSELKKLKKLEGNELQ
                                                                                                                            1407 AKKKVDDDLGTIEGLEENKKKLLKDMESLSORLEEKA-
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Accession: B43402; A43402
Takahashi, M.; Kawamoto, S.; Adelstein, R.S.
Biol. Chem. 267, 17864-17871, 1992
Title: Evidence for inserted sequences in the head region of nonmuscle myosin specific
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corresponding nucleotide se
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                                                                               533
                                                                                                                                  325 VWWVSQFVKYLIRPQPWLEREIEETTKKLGFKHPVIGVHVR-RTDKV--GTEAAFHPIEE 381
                                                                                                                                                                                                                          431
                                                                                                                                                                                                                                                                 601 FUNQLKELRELYNKQOFQKQOPFETEKIKQKELERKTSELDKLKEEDKR----RMLEQDK 656
                                                                                                                                                                                                                                                                                                              491
                                                                                                                                                                                                                                                                                                                                                    657 L-W----QDRVKQEEERYKFQDEEKEKREE----SVQKCEV--EKKPEIQEKPNKPFH 703
                                                                                                                                                                                                                                                                                                                                                                                                                                      704 OPPEPGKLGGOIPWMYTEKAPLTINOGDVKVVYYRALYPFDARSHDEITIEPGDIIMVDE 763
                                                                                                                                                              SLDDIYYFGGQ----NAH----NQ-----IAVYPHQPRTKEEIPMEPGDIIGVAG
                                                                                                                                                                                                                        382 YMVHVEEHFQLLERRM------KVDKKRVYLATDDPSLLKEAKTKYSNYEFISDNS
                                                                                                                                                                                                                                                                                                              432 ISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIMQTLHPDASANFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212-221/Region: alternatively spliced segment 1 #status experimental 559-593/Region: actin binding #status predicted 632-652/Region: alternatively spliced segment 2 #status experimental 692-714/Region: actin binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                534 NH-----WNGYSKGVNRKLGKTGLYPSYKVREKIETVKYP--TYPEAE 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;122/Modified Site: N6.N6.N6-Trimethyllysine (Lys) #status prediction Site: ATP (Lys) #status predicted 1.184/Binding Site: ATP (Lys) #status predicted 1.1954/Binding Site: Cys #status predicted 1.1954/Binding Site: phosphate (Thr) (covalent) #status predicted 1.1967/Binding Site: phosphate (Ser) (covalent) #status predicted 1.1987/Binding Site: phosphate (Ser) (covalent) #status predicted
                                               273 STGHWSGEVKDKNVQVVELP-IVDSLHPRPPYLPLAVPE--DLADRLLRV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: mRNA
Residues: 1-2007 <TAK>
;Crose-references: GB:M93676; NID:g212448; PIDN:AAA48988.1;
;Note: the sequence of residues 212-221 and 632-652 and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reference number: A43402; MUID:92388144; PMID:1355479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Domain: coiled coil #status predicted <COI>/Region: S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heavy chain-B, neuronal - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contains myosin ATPase (EC 3.6.4.1)
Species: Gallus gallus (chicken)
Date: 31-Dec-1993 #sequence revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .6-2007/Region: light meromyosin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Best Local Similarity
Matches 44; Conserv
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 2, 2004, 08:39:39; Search time 10.5 Seconds (without alignments) 2575.272 Million cell updates/sec Run on:

US-09-971-773-23 3081 1 MRAWTGSWRWIMLILFAWGT......YKVREKIETVKYPTYPEAEK 575 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### STIMMARTES

,	Description	ts2 m alpha- (	ㅁ	Ω		8			Q03410 rattus norv				aquifex	xenop	homo	P30622 homo sapien	rattn	rattr		Q62209 mus musculu			ther	P33175 mus musculu			Q99323 drosophila	Q9jlt0 rattus norv	Q90339 cyprinus ca	œ		~	Ogyfzl aeropyrum p	
SUMMARIES	aı		FUT8_HUMAN		FUT8_PIG		COGS_DROME	MYH9_CHICK		SCP1_MESAU	MYH9 HUMAN	MYHA BOVIN	RASO_AQUAE	ITN1_XENLA	SCP1_HUMAN	REST_HUMAN	ITN1_RAT	MYH9_RAT	OSF1_HUMAN	SCP1_MOUSE	CEP2_HUMAN	DMD_CANFA	RASO_THEAC	KINN_MOUSE	MYHA_HUMAN	CENF HUMAN	MYSN_DROME	MYHA_RAT	MYSS_CYPCA	MYSS CHICK	SPCA_MOUSE			GOG4_HUMAN
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d	* Query Match	97.8	96.9	95.4	93.6	4.3	4.2	4.1	4.1	4.0	4.0	4.0	•	٠	•	•	•	•	٠.	3.8	•	٠	•	•	•	٠	•	•	٠	٠	٠	3.6	3.6	9.6
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014939 homo sapien P70498 rattus norv Q20060 caenorhabdi P49025 mus musculu Q9ukx3 homo sapien P12844 caenorhabdi P12270 homo sapien P28367 bacillus su 067622 aquifex aeo Q9y623 homo sapien Q08378 homo sapien Q08378 homo sapien	,
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# ALIGNMENTS

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ALTERNATIVE PRODUCTS:
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                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send a email to license@isb-sib.ch).
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glucosaminyl-(1->2)-alpha-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->4)-N-acetyl-beta-D-glucosaminyl-(1->4)-[alpha-L-fucosyl-(1->6)]-N-acetyl-beta-D-glucosaminyl-(1->4)-[alpha-L-fucosyl-(1->6)]-PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: Type II membrane protein. Membrane-bound sintla trans cisterane of Golgi (By similarity).
SIMILARITY: Contains 1 SH3 domain.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRAWIGSWRWIMLILFAWGTLLFYIGGHLVRDNDHPDHSTRELSKILAKLERLKQQNEDL
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SH3.BINDING (POTENTIAL)
IMPORTANT FOR DONOR-SUBSTRATE BINDING.
                                                                                                                                                                                                                           InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
PROSITE; PSS0002; SH3; FALSE_NEG.
Transferaes; Glycosyltransferaes; Transmembrane; Signal-anchor; Golgi stack; SH3 domain.
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                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

97.8%; Score 3013; DB.1; Length 575;
Best Local Similarity 97.0%; Pred. No. 1.9e-193;
Matches 558; Conservative 11; Mismatches 6; Indels C
                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
LUMENAL, CATALYTIC (POTENTIAL)
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Q -> E (IN REF. 2).
N -> K (IN REF. 2).
7BE2ED3146E0C45F CRC64;
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575 AA;
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CONFLICT
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TLHPDASANFHSLDDIYYFGGQNAHNQIAVYPHQPRTKEEIPMEPGDIIGVAGNHWNGYS
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Alpha-(1,6)-fucosyltransferase (EC 2.4.1.68) (Glycoprotein 6-alpha-L-fucosyltransferase) (GDP-fucose)
COPP-L-Fuc.N-aceryl-beta-0-Qlucosaminide alpha1,6-fucosyltransferase)
(alpha1-6FucT) (Fucosyltransferase 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Purification and cDNA cloning of GDP-L-Fuc:N-acetyl-beta-D-glucosaminide:alpha1-6 fucosyltransferase (alpha1-6 FucT) from human gastric cancer MKO45 cells.", J. Blochem. 121-67-67-77-77-77-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A sequence motif involved in the donor substrate binding by alphal, 6-fucosyltransferase: the role of the conserved arginine residues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takahashi T., Ikeda Y., Tateishi A., Yamaguchi Y., Ishikawa M.,
Taniguchi N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Embryo;
Callleau A., Balanzino L., Candelier J.J., Oriol R., Mollicone
"Differential splice variants of human FUT8 embryonic cDNA.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE=20275614; PubMed=10814706;
Yamaguchi Y., Ikeda Y., Takahashi T., Ihara H., Tanaka T., S
Vozumi N., Yanagidani S., Inoue S., Fujii J., Taniguchi N.;
Genomic structure and promoter analysis of the human
alpha1,6-fucosyltransferase gene (FUT8).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                       575
                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1), AND FUNCTION.
MEDLINE=97279058; PubMed=9133635;
                                                                                                       KGVNRKLGKTGLYPSYKVREKIETVKYPTYPEAEK
                                                                                                                                                                                                                                                                                          575 AA
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EKEAKDLTELVQRRITYLQNPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRT
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NCBI_TaxID=9913;
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28-FEB-2003 (
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or send an email to license@isb-sib.ch).
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IMPORTANT FOR DONOR SUBSTRATE BINDING.
EVKDKNVGVVELPIVDSLHPRPPYLPLAVPEDLADRLVRVH
GDPAVWWVS -> TPINNLLVITLFPGGLDCTIDTQKIHFV
E (in isoform 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGAKELWFFLQSELKKLKKLEGNELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGEWR
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E (in isoform 2).
/FITEAEVSP 001807.
Missing (in isoform 2).
/FITEAEVSP 001808.
R->A,K: COMPLETE LOSS OF ACTIVITY.
R->A,K: DECREASES ACTIVITY TO 3%.
W, SAE24A93881E18D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; Signal-anchor;
                                     Name=2; Synonyme=Retinal;
Isola@QBYC5-2; Sequence=VSP 001807, VSP 001808;
SIMILARITY: COntains 1 SH3 domain.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.9%; Score 2984; DB 1; Length 575; 96.2%; Pred. No. 1.7e-191; ive 10; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LUMENAL, CATALYTIC (POTENTIAL).
  Bvent=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase, Glycosyltransferase, Transmembran
Golgi stack, SH3 domain, Alternative splicing.
                             Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                           EMBL, D89289; BAA19764.1; --
EMBL, AF038281; AAB92372.2; --
EMBL, Y17979; CAA76983.1; --
EMBL, Y17979; CAA76988.1; --
EMBL, Y17979; CAA76986.1; --
EMBL, Y17979; CAA76986.1; --
EMBL, AB049828; BAB4097.1; --
EMBL, AB049289; CAA76987.1; --
EMBL, AB043257; BAB40929.2; --
EMBL, AB032573; BAA92858.1; --
EMBL, AB032576; BAA92858.1; --
EMBL, AB032576; BAA92858.1; --
EMBL, AB032570; BAA92858.1; JOINED.
EMBL, AB032570; BAA92858.1; JOINED.
EMBL, AB032570; BAA92858.1; JOINED.
EMBL, AB032570; BAA92858.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50002; SH3; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66515 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 602589; -.
InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 96.24
Matches 553; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB032570; BAA92855
EMBL; AB032571; BAA92855
PIR; JC5432; JC5432.
Genew; HGNC:4019; FUT8.
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             Name=1;
IsoId=Q9BYC5-1;
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366 3
575 AA;
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SEQUENCE
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TISSUB-LUNG.

MEDLINE-20523969; PubMed=11070054;

MEDLINE-20523969; PubMed=11070054;

MEDLINE-20523969; PubMed=11070054;

Mattah A., Mattah A., Michalski J.-C., Oriol R.,

Petit J.-M., Julien R.;

"Ancestral exonic organization of FUT8, the gene encoding the alphac-fucosyltransferase, reveals successive peptide domains which suggest a particular three-dimensional core structure for the alphac-fucosyltransferase family.";

Mol. Biol. Evol. 17:1651-1672(2000).

-- FUNCTION: Catalyzes the addition of fucose in alpha 1-6 linkage to the first Globac residue, next to the peptide chains in N-glycans (By similarity).
                                                                                                                                                                       421 YPNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFISQADFLVCTFSSQVCRVAYEIMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVKDKNVQVVELPIVDSLHPR
                                                                                                                                                                                                                                                                                                                                                                                                              GVHVRRTDKVGTEAAFHPIEBYMVHVEEHFQLLERRMKVDKKRVYLATDDPSLLKEAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-(1,6)-fucosyltransferase (RC 2.4.1.68) (Glycoprotein 6-alpha-L-fucosyltransferase) (GDP-fucosoprotein fucosyltransferase) (GDP-fucosoprotein fucosyltransferase) (GDP-L-Pucosoprotein fucosyltransferase) (alpha1-6Fucr) (Fucosyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBCELLUTAR LOCATION: Type II membrane protein. Membrane-bound form in trans cisternae of Golgi (By similarity).
-i- TISSUE SPECIFICITY: Highest expression found in brain. Also found
                                                                                                                                                                                                                                                                           PPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEREIEETTKKLGFKHPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (By similarity).

CATALYTIC ACTIVITY: GDP-L-fucose + N(4)-{N-acetyl-beta-D-glucosaminyl-(1-2)-alpha-D-mannosyl-(1->3)-[N-acetyl-beta-D-glucosaminyl-(1-2)-alpha-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-glucosaminyl-(1->6)]-beta-D-glucosaminyl-(1->6)]-beta-D-glucosaminyl-(1-2)-alpha-D-mannosyl-(1->8)]-beta-D-glucosaminyl-(1-2)-alpha-D-mannosyl-(1->8)]-beta-D-mannosyl-(1->8)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-D-mannosyl-(1->6)]-beta-
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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566-575, AND
TISSUE=Brain;
                                             28-FEB-2003
28-FEB-2003
                                                                 28-FEB-2003
       RESULT 4
FUT8_PIG
ID FUT8_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
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                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                          181 EKEAKDLTELVQRRITYLQNPKDCSKAKKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRT
                                                                                                                                                                                                                                                                                                                                    1 MRPWIGSWRWIMLILFAWGTLLFYIGGHLVRDNDHPDHSSRELSKILAKLERLKQQNEDL
                                                                                                                                                                                                                                                                                                                                                              RRMAESLRIPEGPIDOGTATGRVRVLEEQLVKAKEQIENYKKQARNDLGKDHEILRRRIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 LILESHNWRYATGGWETVFRPVSETCTDRSGVYTGHWSGEIKDKNVQVVELPIVDSLHPR
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                                                                                                                                                                                             PROTEIN)
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                           SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
Transferase; Glycosyltransferase; Transmembrane; Signal-anchor;
Golgi stack; SH3 domain.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE
         SIMILARITY: Contains 1 SH3 domain.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 23
                                                                                                                                                                                                                                                                                   575;
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                                                                                                                                                                                                                                                                FE04C66B8A5BF540 CRC64;
                                                                                                                                                                                                                                    SH3-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                  95.4%; Score 2939; DB 1; 94.4%; Pred. No. 1.6e-188;
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spleen and kidney
                                                                                                              EMBL; AF247186; AAF65460.1; -. InterPro; IPR001452; SH3. PF00018; SH3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              **X MEDLINES-7006976; PubMed=8910378; A MEDLINES-7006976; PubMed=8910378; A MEDLINES-7006976; PubMed=8910378; A Teshima T., Fujii S., Shiba T., Taniguchi N.; Teshima T., Fuzication and cDNA cloning of porcine brain GDP-L-Fuc:N-acetyl-beta-D-glucosaminide alphal-->fucosqltransferase."; J. Biol. Chem. 271:27810-27817 (1996).

**Le FINCTION: Catalyzes the addition of fucose in alpha 1-6 linkage to the first GlonAc residue, next to the peptide chains in N-glycans. The pH optimum is 7.

**C. -CATALYTIC ACTIVITY: GDP-L-fucose + N(4)-{N-acetyl-beta-D-glucosaminyl-(1-2)-alpha-D-mannosyl-(1-3)-beta-D-mannosyl-(1-3)-beta-D-glucosaminyl-(1-2)-alpha-D-mannosyl-(1-3)-N-acetyl-beta-D-glucosaminyl-(1-2)-alpha-D-mannosyl-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)-(1-3)
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SIGNAL-ANGHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
LUMENAL, CATALYTIC (POTENTIAL).
                                                                                                                                                                                               Alpha-(1,6)-fucosyltransferase (EC 2.4.1.68) (Glycoprotein 6-alpha-L-fucosyltransferase) (GDP-fucose-glycoprotein fucosyltransferase) (GDP-L-Fuc:N-acetyl-beta-D-glucosaminide alphal,6-fucosyltransferase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50002; SH3; 1.
Transferase; Glycosyltransferase; Transmembrane; Signal-anchor; Golgi stack; SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., SEQUENCE OF 102-130; 333-344; 402-415 AND 566-575, AND FUNCTION.
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SH3-BINDING (POTENTIAL)
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Pred. No. 6.5e-185;
                                                                                (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
575 AA
                                                                                                                                                                                                                                                                                                                                         (alpha1-6FucT) (Fucosyltransferase 8)
PRT;
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InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
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STANDARD;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                              scrofa (Pig)
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                                                       1 MRPWTGSWRWIMLILFAWGTLLFYIGGHLVRDNDHSDHSSRELSKILAKLERLKQQNEDL
                                                                                                                                                                                                                                                            LALESHNWRYATGGWETVFRPVSETCTDRSGSSTGHWAGGEVKDKNVQVVELPIVDSVHPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 ALHPDASANFRSLDDIYYFGGPNAHNQIAIYPHQPRTEGEIPMEPGDIIGVAGNHWDGYP
                                1 MRAWIGSWRWIMLILFAWGTLLFYIGGHLVRDNDHPDHSSRELSKILAKLERLKQQNEDL
                                                                                                   RRMAESLRIPEGPIDOGTATGRVRVLEEQLVKAKEQIENYKKQARNDLGKDHEILRRRIE
                                                                                                                                                                                                                                          EKEAKDLTELVQRRITYLQNPKDCSKARKLVCNINKGCGYGCQLHHVVYYCFMIAYGTQRT
                                                                                                                                                                                                                                                                                                              LILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVKDKNVQVVELPIVDSLHPR
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Gaps
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25; Indels
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Schizosaccharomycetales, Schizosaccharomycetaceae,
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16; Mismatches
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MEDLINE=21848401; PubMed=11859360;
534; Conservative
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               Weltjens I., Vanstreells E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Back A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmernann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Doga R.R., Cruzado L., Jimenz J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Chrift L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hiracka Y.;
"Large-scale screening of intracellular protein localization in living fission yeast cells by the use of a GFP-fusion genomic DNA library."; genes Cells 5:169-190(2000).
-!- FUNCTION: AFTER THE OWNET OF MITOSIS, AT MID- TO LATE ANAPHASE, CO-LOCALIZES WITH 'THE MEDIAL ACTIN RING: MAY PLAY A ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DHPDHSSRELSKILAKLERLKQQNEDLRRMAESLRIPEGPIDQGTATGRVRVLEEQLVKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jimenez M., Petit T., Gancedo C., Goday C.;
"The alm1+ gene from Schizosaccharomyces pombe encodes a coiled-coil protein that associates with the medial region during mitosis.";
Mol. Gene. 262:921-930(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ding D.-Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
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ches 226; Indels 108;
Grymonprez B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.3%; Score 133; DB 1; Length 1727; 21.2%; Pred. No. 0.66; ive 74; Mismatches 226; Indels 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 495-1727 FROM N.A., AND CHARACTERIZATION.
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   Woodward J., Volckaert G., Aert R., Robben J.,
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EMBL; AF010473; AAB654[6.1; ALT_INIT.
EMBL; AB028012; BAA873[6.1; -.
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GeneDB_SPombe; SPAC1
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RADIENTE R.G., Roberter S.E., Li P.W., Hookkins R.A., Galle R.F.,

RADIENTE R.G., Roberter S.E., Richards A., Ashburner M., Henderson S.N.,

RADIENTE, R.G., Roberter E.G., Helt G., Champe M., Pfeiffer B.D.,

RADII J.F., Adpayani A., R.H.-C., Baralle M.P., Relation C.R., Miklos G.L.G.,

RADII W. R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RADII W. R.M., Cawley B.C., Berman B.P., Bhandari D., Bolshakov S.,

RADIEW R.M., Cawley S., Derman B.P., Brandari D., Bolshakov S.,

RADIEW R.M., Cawley S., Danle C., Davenport L.B., Davies P.,

RADIENTS R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RADIENT J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RADIOS B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RADIENT S.M., Evangelista C.C., Ferrara C., Ferriera S., Fleischmann W.,

RADIENT R.M., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RADIENT R.M., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RADIENT R.M., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RADIENT R.M., Moylen D.R., Diet M. Muzhy B., Muzhy D.M., Muzhy D.M., Nusskern D.R., Palazolo M., Pittman G.S., Pollard J., Puri V., Reese M.G.,

RADIENT R.M., Nelson K.A., Nixon K., Nusskern D.R., Puri V., Reese M.G.,

RADIENT R.M., Pelson K.A., Nixon K., Nusskern D.R., Puri V., Reese M.G.,

RADIENT R.M., Pelson K.A., Nixon K., Nusskern D.R., Puri V., Reese M.G.,

RADIENT R.M., Pelson K.A., Nixon K., Nusskern D., Puri V., Reese M.G.,

RADIENT R.M., Pelson K.A., Nixon K., Nusskern D., Puri V., Reese M.G.,

RADIENT R.M., Pelson K.A., Nixon K., Nusskern D., Puri V., Pelson D.M.,

RADIENT R.M., Pelson K.A., Nixon K., Nusskern D., Puri V., Reese M.G.,

Response M. R. R. Rodier R. R., Ro
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SQLQTEKAAVKKLENSNEEYKRHNQEILLSL-NSSTSTSSDASRLK----NELVSKE-- 1330
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                                                 DLTELVORRITYLONPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILES
                                                                                                     --AQNQSKIEQLEL
                                                                                                                                                      QNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVKDKNVQVVELPIVDSLHPRPPYLP
                                                                                                                                                                                                          1374 KNITKLA-AAWRIKYEQVVNKSLEKHNQIRQQLSQKTSELEAKVAECHQLNEQLNKPSATP
                                                                                                                                                                                                                                                              LAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEREIEETTKKLGFKHPVIGVHVR
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28-FFB-2003 (Rel. 41, Created)
28-FB-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Putative conserved oligomeric Golgi complex subunit 5 (Four way stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxID=7227,
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Shue B.C., Siden-Kiamos I., Simpson M.; Skupski M.P., Smith T., Shien B.C., Siden-Kiamos I., Simpson M.; Skupski M.P., Smith T., Spier B., Spradling A.C., Stapleton M.; Strong R., Sun E., Svirskas R., Tector C., Turner R., Wenter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Yeh R.-F., Zavori J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Shirh H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                             STRAIN BERKeley; TISSUE=Embryo; MEDLINE=22426066; PubMed=12537569; Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M., Garlson J.W., Erokstein P., Yu C., Champe M., Gorge R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H., Rubin G.M., Celniker S.E.; A Drosophila full-length cDNA resource."; Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
-!- FUNCTION: Required for normal Golgi function (By similarity).
-!- SUBUNIT: Component of the conserved oligomeric Golgi complex which is composed of eight different subunits and is required for normal Golgi morphology and localization (By similarity).
-!- SUBCELLULAR LOCATION: Golgi (By similarity).
-!- SINILARITY: BELONGS TO THE COG5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 SVLNKSPTHNVSKPAPSRGPGKTPOLTTTONPR--AKFWKSLHWLLYDELFBTCTQIKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 KTALEQINQFGYTSESSDQCIPQRFWQQVQALRKSFDECPQHVTQTLQEGLSKLLTSAR
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20.7%; Pred. No. 0.33;
ive 98; Mismatches 212; Indels 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.ish-r
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ProDom; PD000355; myosin_head; 1.
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                                                                         FIRVASTELSAALIDSRLTNAIANVFAACGKELCTKLEAQIKLGADSKQV---VDLPNLO 462
                                                                                                                                                                                                                                QADFLVCTFSSQVCRVAYE----IMQTLHPDASANFHSLD------DIYYFGGQNAH 505
                                                                                                                                                                                                                                                           ---EEHFQLLERRMKV--DKKRVYLATDDPSLL 414
                                                                                                                                                                           -----YYKDSVRRMLSDLHVHFEKTPGTAREIISRSLE 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (WHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEFILDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

SIMILARITY: Contains I myosin-like globular head domain.

SIMILARITY: Contains I IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning of the cDNA encoding the myosin heavy chain of a vertebrate cellular myosin.";

Proc. Natl. Acad. Sci. U.S.A. 86:7726-7730(1989).

-!- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS,
CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
CAPPING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, nonmuscle (Cellular myosin heavy chain) (NWMHC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Intestinal epithelium;
MEDLINE=90046668; PubMed=2813355;
Shohet R.V., Conti M.A., Kawamoto S., Preston Y.A., Brill D.A.,
Adelstein R.S.;
                                                                                                                              KEAKTKYSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHF---
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Pfam; PF00612; IQ; 1.
Pfam; PR00063; Wyosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHBAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, P10587; 1BR2.
InterPro; DPR000048; IQ region.
InterPro; IPR001609; myosin head.
InterPro; IPR004009; Myosin_N.
                               ----GTEAAFHPIEEYMVHV---
                                                                                                                                                           SOONTOLANVLF-----
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                                                                                                                                                                                                                                                                                                                                     NQIAVYPHQPRTKE 519
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HHIALFDDKQMTKK 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                 415
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P14105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 RSGLSTGHWSGEVKDKNV--QVVELPIVDSLHPRPPYLPLAVPEDLADRL--LRVHGDPA 324
                                                                                                                                                                                                                                                                                                                                                                                           98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 ADEILLDLGHHERSIMTDLYYLSQTDGAGEWREKEAKDLTELVQRRITYLQNPKDCSKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 KLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQNWRYATGGWETVFRPVSETCTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1233 VKVLLQGKGDAEHKRKKVDAQLQELQVKFTEGER-----VKTELAERVNKLQVELDNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 VWWVSQ----FVKYLIRPQPWLEREI-----EETTKKLGFKHPVIGVHVRRTDKVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373 BAAFHPIEEYMVHVEEHFQLLERRMKVDKKRVYLATDDPSLLKEAKTKYSNYEFISDNSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                433 SWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIMQTLHPDASANFHS
                                                                                                                                                                                                                                                                                                                                                                                           42 ELSKILAKLE-RLKQONEDLRRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIE--
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ::| :| | : ||:: | ::|
EDEKNALKEQLEESEEAKRNLEKQISVLQQQAV------EARKKMD----
                                                                                                                                                                                                                                                                                                     Length 1959;
                                                                                                                                                                                                                ALKYLATION (SH-1) (POTENTIAL)
ALKYLATION (SH-2) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                         MW; A75C86086FD3A1A1 CRC64;
                                                        Myosin; ATP-binding; Calmodulin-binding; Actin-binding; Colled coil; Alkylation; Multigene family.

DOMAIN

1 778

MYOSIN HEAD-LIKE.
                                                                                                                          1Q.
COLLED COLL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                       4.1%; Score 127.5; DB 1;
19.8%; Pred. No. 1.8;
ve 79; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   003410;
01-UNN-1994 (Rel. 29, Created)
15-ULL-1998 (Rel. 36, East sequence update)
Synaptonemal complex protein 1 (SCP-1 protein)
SYCP1 OR SCP1
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SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                AA;
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Matches 110; Conserv
                                                                                                                                                                                                                   694
704
1959
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                                                                                                                                                                                                                                                              SEQUENCE
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845 AA;
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(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                 SCP1 OR SYN1.
                                                                                                                                                                                                                                                                                                                                                                                          Mesocricetus
                                                                                                                                                                                                                                                         01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moens P.B.;
                                                                                                                                                                                                                                MESAU
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SEQUENCE
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SCP1 MESAU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 NPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQNWRYATGGWETVF 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 K-----KOARNDLGKD-----HEILRRRIENGAKELWFFLOSELKKLKKLEGNELQR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 HAD-----EILLDLGHHERSIMTDLYYL--SQTDGAGEWREKEAKDLTELVQRRITYLQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 EVNNKENQVSLLLIQSTEKENKMKDLTFLLEESRDKANQLEEK-----TKLQDENLKELN 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278 --SGEVKD----KNVQVVELPIVDSLHPRPPYLPLAVPEDLADRLLRVHG-DPAVWWVSQ 330
                                                                                                                                                                                    SYNAPTONEMAL COMPLEXES, BETWEEN LATERAL ELEMENTS IN THE NUCLEUS.
COUDD OULY WHERE THE CHROMOSOME CORES ARE SYNAPEDED. ITS N-TERNINUS
IS FOUND TOWARDS THE CENTRE OF THE SYNAPTONEMAL COMPLEX WHILE THE
C-TERMINUS EXTENDS WELL INTO THE LATERAL DOMAIN OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316 EKKÜHLTS----EEDLQIAT---KTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415 KKSSELEEMTKFKNNKEVELEELKTI-----LÄEDQKLLÜEKKQVEKLAEELQGKEĞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.1%; Score 127; DB 1; Length 997;
20.3%; Pred. No. 0.8;
ive 86; Mismatches 188; Indels 138; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELSKILAKLERLKQQNEDLRRMAESLRIPEGPIDQGTATGR-VRVLEEQLVKAKEQIENY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLLED COIL (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
ARG/LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                                                   DOMAIN: CONSISTS OF AN ALPHA-HELICAL STRETCH OF 700 AA RESIDUES, FLANKED BY N- AND C-TERMINAL GLOBULAR DOMAINS. THE C-TERMINAL DOMAIN HAS DNA-BINDING CAPACITY.

CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT WAS CORRECTED IN POSITION 6 TO MAXIMIZE THE SIMILARITY WITH THE OTHER SPECIES SYCPI SEQUENCES.
                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: Testis.
DEVELOPMENTAL STAGE: EXPRESSED EXCLUSIVELY IN MEIOTIC PROPHASE
                                                       Meuwissen R.L.J., Offenberg H.H., Dietrich A.J., Riesewijk A., Iersel M., Heyting C.; "A coiled-coil related protein specific for synapsed regions of
                                        MEDLINE=93099884; PubMed=1464329;
Meuwissen R.L.J., Offenberg H.H., Dietrich A.J., Riesewijk A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: MAJOR COMPONENT OF THE TRANSVERSE FILAMENTS OF SYNAPTONEMAL COMPLEXES (SCS), PORED BETWEEN HOMOLOGOUS CHROWOSOMES DIRING MEIOTIC PROPHASE. SUBSCELLULAR LOCATION: NUCLEAR. IN TRIPARTITE SEGMENTS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, X67805; CAA48006.1; ALT FRAME.
Nuclear protein; Meiosis; Cell division; Phosphorylation;
DNA-binding; Colled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         990 ARG/LYS-RICH (BASIC).
116511 MW; 229D59823FD684BE CRC64;
                                                                                                 meiotic prophase chromosomes.";
EMBO J. 11:5091-5100(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105; Conservative
                                                                                                                                                                                                                                               SYNAPTONEMAL COMPLEX.
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905
990
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902
982
997 AA;
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DOMAIN:
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Best Local S
Matches 105
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331 FVKYLI--RPQPWLEREIEETTKKLGFKHPVIGVHVRRTDKVGTEAAFHPIEEYMVHVEE 388
                                         448
                                                                                                                                                                            DMLLLE-----NKKLVQEASDMVLELKKHQEDIINCKKQEERMLKQIETLEEK--EMNLR 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Synaptonemal complex proteins: occurrence, epitope mapping and chromosome disjunction.";

1. Cell Sci. 107:2749-2760(1944).

2. Cell Sci. 107:2749-2760(1944).

2. Cell Sci. 107:2749-2760(1944).

3. Vell Sci. 107:2749-2760(1944).

4. FUNCTION: MAJOR COMPLEXES (SCS), FORMED BETWEEN HOMOLOGOUS CHROMOSOMES DURING MEIOTIC PROPHASE (BY SIMILARITY). HAS NON-SPECIFIC DNA BINDING MEIOTIC PROPHASE (BY SIMILARITY). HAS NON-SPECIFIC DNA BINDING NUCLEAR. IN TRIPARTITE SEGMENTS OF SYNAPTONEMAL COMPLEXES, BETWEEN LATERAL ELEMENTS IN THE NUCLEUS. FOUND ONLY WHERE THE CHROMOSOME CORES ARE SYNAPTONEMAL COMPLEX WHILE THE C-TERMINUS EXTENDS WELL INTO THE LATERAL DOMAIN OF THE
                                                                                                                               389 HFOLLERRMKVDKKRVYLATDDPSLLKEAKTKYSNYEFISDNSISWSAGLHNRYTENSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYNAPTONEMAL COMPLEX.
DOMAIN: CONSISTS OF AN ALPHA-HELICAL STRETCH OF 700 AA RESIDUES,
FLANKED BY N- AND C-TERMINAL GLOBULAR DOMAINS, THE C-TERMINAL
DOMAIN HAS DNA-BINDING CAPACITY (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Meiotic chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dobson M.J., Pearlman R.E., Karaiskakis A., Spyropoulos B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuclear protein; Meiosis; Cell division; Phosphorylation; DNA-binding; Colled coll.
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NUCLEAR LOCALIZATION SIGNAL
NUCLEAR LOCALIZATION SIGNAL
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                                                                                                                                                                                                                                                                      449 GVILDI--HFLSQADFLVCTF--SSQVCR-VAYEIMQ 480
                                                                                                                                                                                                                                                                                                                   DELESVRKEFIQQGDEVKCKLDKSEENARSIEYEVLK 611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Synaptonemal complex protein 1 (SCP-1 protein)
synaptic complex protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 124.5; DE
Pred. No. 0.95;
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MEDLINE=95181577; PubMed=7876343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW.
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                                                                                                                     ---SKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQ--NWRYATGGWETVF 259
                                                                                                                                                                                                                                                                     -----KEKOMKILENKCNNLRKOA---ENKS 486
                                                                                                                                                                                                                                                                                                        RPVSETCTDRSGLSTGHWSGEVKDKNVQVVEL------PIVDSLHPRPPYL 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20057165; PubMed=10591208; Bruskiewich R., Beare D.M., ADIMAM I., Hunt A.R., Collins J.E., Bruskiewich R., Babbage A.K., ADIMAM I., Hunt A.R., Collins J.E., Bruskiewich R., Babbage A.K., Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P., Bardey S.E., Bridgeman A.M., Buck D., Burgess J., Bridgeman A.M., Buck D., Burgess J., Burdey S.E., Coller R.E., Connor R., Clegs S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Corroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson B., Dawson E., Dodsworth S.J., Durbin R.M., Ellington A.G., Brans K.L., Few J.M., Fleming K., French L., Garner A.A., Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C., Anna F. Jones M.C., Kershaw J., Kimberley A.M., King A., Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M., Martyn I.D., Mashreghi-Mohammadi M., Mathews L.H., Mccann O.T., Martyn I.D., Mashreghi-Mohammadi M., Mille S.A., Mortimore B.J.C.T., Andell C.N., Pavitt R., Paurs A.V., Pearson D., Phillimore B.J.C.T., Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T., Scherlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M., Vaudin M., Wall M., Walliams E., Williams S.A., Williams D., Williams E., Williams E., Williams E., Williams E., Williams D., Williams E., Williams E., Williams E., Williams D., Williams E., Williams E., Williams E., Williams D., Williams D., Williams E., Williams E., Williams D., Williams E., Williams E.
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                                                      : : | : | : | : | : | KYIEELHQENKALKKKS-SAESKQLNAYEIKVNKLQLELESAKQKFQEMTDNYQKE----
                                   ELSKILAKLERLKOONEDLRRMAESLRIPEGPID -- OGTATGRVRVLEEQLVKAKEQIEN
                                                                                                   YKKQARNDLGKDHEILRRRIENGAKELWFFLQSELKKLK-----KLEGNELQRHADE
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Gaps
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P35579; 060805;
01-JUN-1994 (Rel. 29, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Myosin heavy chain, nonmuscle type A (Cellular myosin heavy chain, type A) (Nonmuscle myosin heavy chain, MYH9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
84; Mismatches 157; Indels 113;
                                                                                                                                                                                                                                                                      449 KSEENARSIECEVLK------
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652 KLEKENTAILKDKKDK 667
   Conservative
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   82;
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Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N., Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S., Kahibuya K., Yoshizaki Y., Aoki N., Mitsuyama S., Do A., Do Dorman A., Fang F., Chu L., Crabbree J., Deschamps S., Lo A., Do T., Lewis J., Lin S., P., Luh P., Malaj E., Nguyen I., Pao H.I., Lewis J., Lins S., Lin R., P., Ren C., Shauli S., Sloan D., Song L., Mang Q., Wang Y., Wang Z., White J., Miller N., Minx P., Song L., Annong C., Chisoco S., Murray J., Miller N., Minx P., Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J., Athion R., Johnson D., Bemis G., Benley D., Bradshaw H., Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J., Athios K., Kemp K., Latrelle P., Layman D., Ozersky P., Rohlfing T., Scheet P., Walker C., Wamasley A., Wohldmann D., Pepin K., Nelson J., Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P., Milkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20428192; PubMed=10973259;
MEDLINE=20428192; PubMed=10973259;
Seri M., Cusano M., Gangarossa S., Caridi G., Bordo D., Lo Nigro C.,
Ghiggeri G.M., Ravazzolo R., Savion M., Del Vecchio M., d'Apolito M.,
Iolascon A., Zelante L.L., Savoia A., Balduini C.L., Noris P.,
Magrini U., Belletti S., Heath K.E., Babcock M., Glucksman M.J.,
Aliprandis E., Bizzaro N., Desnick R.J., Martignetti J.A.,
"Mutations in MYH9 result in the May-Hegglin anomaly, and Fechtner and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT DFNA17 HIS-705.
MEDLINE=20489856; PubMed=11023810;
Lalwani A.K., Goldstein J.A., Kelley M.J., Luxford W., Castelein C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Human nonsyndromic hereditary deafness DFNA17 is due to a mutation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simons M., Wang M., McBride O.W., Kawamoto S., Yamakawa K., Gdula D., Adelstein R.S., Weir L.; "Human nommuscle myosin heavy chains are encoded by two genes located on different chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toothaker L.E., Gonzalez D.A., Tung N., Lemons R.S., le Beau M.M., Arnaout M.A., Clayton E.K., Teren D.G., "Cellular myosin heavy chain in human leukocytes: isolation of 5' cDNs clones, characterization of the protein, chromosomal localization, and uprespulation during myeloid differentiation."; Blood 78:1826-1833(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE=90138958; PubMed=1967836;
Saez C.G., Myers J.C., Shows T.B., Leinwand L.A.;
"Human nonmuscle myosin heavy chain mRNA: generation of diversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS MHA ILE-1155 AND LYS-1841.
MEDLINE-20428193; PubMad-10973560;
Kelley M.J., Jawien W. Ortel T.L., Korczak J.F.;
"Mutation of MYH9, encoding non-muscle myosin heavy chain A, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS MHA/FTNS/SBS S.YS-93; CYS-702; CYS-1165; HIS-1424 AND
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Proc. Natl. Acad. Sci. U.S.A. 87:1164-1168(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The DNA sequence of human chromosome 22.";
Nature 402:489-495(1993).
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SEQUENCE OF 1-1337 FROW N.A.
MEDLINE=92003925; PubMed=1912569;
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Nat. Genet. 26:106-108(2000)
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                                             -!- SUBUNIT.

CAPPING.

-!- SUBUNIT.

CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2

REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEDTAREPIDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

-!- DISEASE: DEFECTS IN MYH9 ARE THE CAUSE OF MAY-HEGGLIN ANOMALY (MHA), AN AUTOSOWAL DOMINANT MACROTHROMBOCYTOPENIA CHARACTERIZED BY THROMBOCYTOPENIA, GIANT PLATELETS AND LEUKOCYTE INCLUSIONS.

-!- DISEASE: DEFECTS IN MYH9 ARE THE CAUSE OF SECHTWER SYNDROME (FTNS), AN AUTOSOWAL DOMINANT MACROTHROMBOCYTOPENIA CHARACTERIZED BY THROMBOCYTOPENIA, GIANT PLATELETS AND LEUKOCYTE INCLUSIONS.

WITH ADDITIONAL ALPORT-LIKE CLINICAL FEATURES OF SENSORINEURAL DEFENSES; CATARACTS AND NEPHRITIS.

-!- DISEASE: DEFECTS IN MYH9 ARE THE CAUSE OF SEBASTIAN SYNDROME (SBS), AN AUTOSOWAL DOMINANT MACROTHROMBOCYTOPENIA CHARACTERIZED BY TROMBOCYTOPENIA, GIANT PLATELETS AND LEUKOCYTE INCLUSIONS.

-!- DISEASE: DEFECTS IN MYH9 ARE THE CAUSE OF AN AUTOSOWAL DOMINANT FORM OF NONSYNDROMIS SINGERISELED BY PROCEEDSIVE HEARING IMPAIRMENT AND
FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS
                 CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 1 myosin-like globular head domain. SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myosin; ATP-binding; Calmodulin-binding; Actin-binding;
Coiled coil; Alkylation; Multigene family; Disease mutation;
Deafness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IQ.
COILED COIL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALKYLATION (SH-1)
ALKYLATION (SH-2)
N -> K (IN MHA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005860; C:non-muscle myosin; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000048; IQ region.
InterPro; IPR04009; Myosin_head.
InterPro; IPR04009; Myosin_N.
InterPro; IPR002028; Myosin_tail.
InterPro; IPR002017; Spectrin.
Pfam; PF00612; IQ; 1.
Pfam; PF00183; Myosin_N; 1.
Pfam; PF001576; Myosin_tail; 1.
Pfam; PR00193; MYOSINHEAVY.
PRODOM: PP000195; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                          COCHLEOSACCULAR DEGENERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z82215; CAB05105.1; -.
EMBL; M81105; AAA59888.1; -.
EMBL; M69180; AAA61765.1; -.
EMBL; M11013; AAA36349.1; -.
PIR; A61211; A61231.
HSSP; P10587; 1BR2.
Genew; HGNC:7579; MXH9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MYSc, 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00015; IQ;
SMART; SM00242; MYSC
PROSITE; PS50096; IQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
MOD_RES
VARIANT
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NP BIND
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: | : : | | : : | | : | 1397 L----SQRHEEKVAAYDKLEKTKTRILQQELDDLL-VDLDHQRQSACNLEKKQKK---FDQ 1448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1227 -GELANBVKVLLQGKGDSEHKRKKVEAQLQELQVKFNEGER------VRTELADKVTK- 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1278 ------GSDSKSSKLTKDFS 1304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 GNELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGEWREKEAKDLTELVQRRITYLQNP 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 KDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQNWRYATGGWETVFRP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 VSETCTDRSGLSTGHWSGEVKDKNV--QVVELPIVDSLHPRPPYLPLAVPEDLADRLLRV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          438 L-HNRYTENSLRGVILDIHFLSQADFLVCTFSSQVC-RVAYBIMQTLHPDASANFHSLDD 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | :: : | | :: : | | :: : | | :: : | | :: : | | :: : | | :: : | | :: : | | :: : | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 HGDPAVWWVSQFVKYLIRPQPWLBRBIBETTKKLGFKHPVIGVHVRRTDKVGTEAA--FH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378 PIEEYMVHVEEHFQLLERRMKVDKKRVYLATDDPSLLKEAKTKYSNYEFISDNSISWSAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 DNDHPDHSSRELSKILAKLERLKQQ----NEDLRRMAESLRIPEGPIDQGTATGRVRVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 124.5; DB 1; Length 1960;
; Pred. No. 2.8;
95; Mismatches 191; Indels 161; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain, type B) (Nonmuscle myosin heavy chain, type B) (Nonmuscle myosin heavy chain, Nonmuscle myosin heavy chain.B) (Nonmuscle myosin heavy chain.B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTIGHTON 10797.
EAI -> RGH (IN REF. 3).
T -> S (IN REF. 3).
T -> M (IN REF. 4).
C -> Y (IN REF. 4).
KG -> GR (IN REF. 4).
/FTIG=VAR 010791.

R -> C (IN FTNS).

/FTIG=VAR 010792.

R -> H (IN DFNA17).
                                                                                                                                                                                                                                                                                                                                                                            /FTId=VAR 010795.
D -> H (IN FTNS).
/FTId=VAR 010796.
E -> K (IN MHA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 19.03
Matches 105; Conservative
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-!- FUNCTION: Involved in DNA double-strand break repair (DSBR). The rad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mrell by unwinding and/or repositioning DNA ends into the mrell active site (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF_00449; -; 1.
InterPro; IPR003439; ABC transporter.
InterPro; IPR004592; SbcC.
InterPro; IPR004501; SpcCrin.
Pfam; PF04430; DUF498; 1.
TIGRRAMs; TIGR00618; Bbcc; 1.
DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.
NP BIND 32 39 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.9%; Score 120.5; DB 1; Length 978;
13.2%; Pred. No. 2.1;
ive 80; Mismatches 161; Indels 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: Forms a complex with mre11 (By similarity).
-!- SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 39 ATP (BY SIMILARITY).
160 826 COILED COIL (POTENTIAL).
978 AA; 115897 MW; 9BOF2BF51ADD1151 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable DNA double-strand break repair rad50 AFPase.
Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 DHPDHSSRELSKILAKLERLKOONEDLRRMAESL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  978 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98196666; PubMed=9537320;
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                                                                                                                                                  148 HADEILLDLGHHERSIMTDL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                               101 KKOARNDLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             1487 S 1487
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                                                                                                                                                                                                                                                                     188 T 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RA50 AQUAE
O67124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=VF5;
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ID RASO A

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DT 16-OCT

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CC A

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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain cortex,
MEDLINE=95301542; PubMed=7782316;
MEDLINE=95301542; PubMed=7782316;
MEDLINE=95301542; PubMed=7782316;
MEDLINE=95301542; PubMed=7782316;
MEDLINE=95301542; PubMed=7782316;
MEDLINE=95301542;
MEDLINE=9530154232;
MEDLINE=95301542;
MEDLINE=95301542;
MEDLINE=95301542;
MEDLINE=95301542;
MEDLINE=95301542;
MEDLINE=95301542;
MEDLINE=9530154232142;
MEDLINE=95301542;
MEDLINE=9530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY ELAIN SUBUNITS (WEC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUR REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHRACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

SIMILARITY: Contains 1 myosin-like globular head domain.

SIMILARITY: Contains 1 Q domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                        Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                        complete cds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 1976;
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ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229097 MW; 6144354451C0F790 CRC64;
                                                                                                                                                                                                                                      Ohara M., Ishiguro N., Shinagawa M.;
"Bos taurus nonmuscle myosin heavy chain B mRNA, complet
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myosin, ATP-binding; Calmodulin-binding; Actin-binding; Coiled coil; Alkylation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IQ.
COLLED COIL (POTENTIAL).
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25.4%; Pred. No. 2.9;
iive 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001044; IQ region.
InterPro; IPR001609; myosin_head.
InterPro; IPR0040609; myosin_head.
InterPro; IPR004090; Myosin_N.
InterPro; IPR0040928; Myosin_Lail.
InterPro; IPR00401; Spectrin.
Pfam; PF001612; IQ; 1.
Pfam; PF00163; myosin_head; 1.
Pfam; PF01576; Myosin_Lail; 1.
ProDom; PD00035; myosin_head; 1.
SMART; SM00015; Myosin_head; 1.
SMART; SM00015; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB022023; BAA36494.1; -.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 204-302 FROM N.A.
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                                                                                                                   Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50096; IQ;
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1976 AA;
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Matches 46; Conserv
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                     NCBI_TaxID=9913;
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SEQUENCE
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72

Gaps

us-09-971-773-23.rsp

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112
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                                                                                                                                                                                                                                                                                                                                                      247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294
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                                                                                                                                                                                                                                                                                                                                                                                                          458 KELERE---LKEREL------HYHAHMVASYLSPGDTCPVCGIYRGKALEN-- 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     602 HKAOTELELLKEKIREKSRLVKEFKELYRVERLEDYEESLKEEINYINSKLOEIEEKEKK 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :: | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
                                                                                                                                               354 ELSQLSSSLKEKERYEQAKQEFEDLSERVEKG-KKLVAETEEKLEKIKELFSEEEYTSL
                                                                                                                                                                                                                                                                          413 KOMKBRILIVELQRKIKELKEKEGQIEN--LTQKY------KEKKKVHEKVINEL
                                                                                                                                                                                                                                                                                                                                                      196 TYLQNPKDCSKARKLVCNINKGCGYGCQLH-HVVYCFM-----IAYGTQRTLILESQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  542 EKLRNEVEELRKEIPENLKERIKKLEELRIEKEKLEHKLNKYRKALEDROKOKEEAQAKL
                                                                                                                    --EILRRRIENGAKELWFFLQSELKKLKKLEGN-----
                                                                                                                                                                                                                                  144 -----ELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGEWREKEAKDLTELVQRRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 WRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVKDKOVVELPI------V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSLHPRPPYLPLAVPEDLADRL-----LRVHGDPAVWWVSQFVKYLIRPQPWLER----
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamabhai M., Hoffman N.G., Hardison N.L., McPherson P.S.,
PIDOGTATGRVRVLEEQLVKAKEQI -----ENYKKQARNDLGKDH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEEHF-QLLERRMKVDKKRVYLATDDPSLLKEAKTK 420
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Last annotation update)
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MEDLINE=99030416; PubMed=9813051;
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28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last ann
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NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325 VWWVSQFVKYLIRPQPWLEREIEETTKKLGFKHPVIGVHVR-RTDKV--GTEAAFHPIEE 381
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EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
LYS/LEU/GLU/ARG/GLN-RICH (POTICE COILED COIL (POTENTIAL).
SH3 1.
SH3 2.
SH3 3.
SH3 4.
                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                               3.9%; Score 119.5; DB 1;
20.6%; Pred. No. 3.5;
ive 82; Mismatches 174;
                                        Interpro; IPR002048; EF-hand.
Interpro; IPR000021; BF915, homology.
Interpro; IPR000108; Neu_Gyt_fact_2.
Interpro; IPR0001452; SH3.
                                                                                                                                                                                                          SH3 domain; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                     82;
                                                                                                                                       SMART; SM00054; EFH; 2.
SMART; SM00027; EH; 2.
SMART; SM00326; SH3; 5.
PROSITE; PS00018; EF HAND; 2.
PROSITE; PS50001; EH; 2.
PROSITE; PS50002; SH3; 5.
           EMBL; AF032118; AAC73068.1;
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                                                                                                                                                                                                                                                                                                                                                                            20.68;
                                                                                   Pfam; PF00036; efhand; 2.
Pfam; PF00018; SH3; 5.
PRINTS; PR00499; P67PHOX.
PRINTS; PR00452; SH3DOMAIN.
                                                                                                                                 SH3; 5.
                                                                                                                                                                                                                                                                                                                                                                             dest Local Similarity 20.6
Matches 121; Conservative
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1122
1198
                                HSSP; P29355; 1SEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Okuyama A., Nishimune Y.,

Okuyama A., Nishimune Y.,

T. Assignment of synaptonemal complex protein 1 (SCP1) to human chromosome 1p13 by fluorescence in situ hybridization and its expression in the testis.";

Cytogenet. Cell Genet. 78:103-104(1997).

Cytogenet. Cell Genet. 78:103-104(1997).

CHROMOSOMES DURING MEIOTIC PROPHASE.

CHROMOSOMES DURING MEIOTIC PROPHASE.

CHROMOSOMES DURING MEIOTIC PROPHASE.

SYNAPTONEMAL COMPLEXES, BETWEEN LATERAL ELEMENTS OF SYNAPTONEMAL COMPLEXES.

FOUND ONLY WHERE THE CHROMOSOME CORES ARE SYNAPSED. ITS N-TERMINUS IS FOUND TOWARDS THE CROTRES OF THE SYNAPTONEMAL COMPLEX WHILE THE CA-TERMINUS EXTERNINUS EXTERN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: CONSISTS OF AN ALPHA-HELICAL STRETCH OF 700 AA RESIDUES, FLANKED BY N- AND C-TERMINAL GLOBULAR DOMAINS. THE C-TERMINAL DOMAIN HAS DNA-BINDING CAPACITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98037449; PubMed-9371398;
Kondoh N., Nishina Y., Tsuchida J., Koga M., Tanaka H., Uchida K.,
Inazawa J., Taketo M., Nozaki M., Nojima H., Matsumiya K., Namiki
                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                           805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Human synaptonemal complex protein 1 (SCP1): isolation and characterization of the cDNA and chromosomal localization of
                           3764 SOTGEPGWLG----GELKGKTGWFPA-NYAERMPESEFPSTTKPAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Meuwissen R.L.J., Meerts I., Hoovers J.M.N., Leschot N.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GG; GO:0005716; C:synaptonemal complex; TAS.
GO; GO:0003677; F:DNA binding activity; TAS.
GO; GO:0007121; P:meiotic recombination; TAS.
GO; GO:0007283; P:spermatogenesis; TAS.
Nuclear protein; Meiosis; TAS.
Nuclear protein; Meiosis; Cell division; Phosphorylation; DNA-binding; Colled coil.
  NH-----WNGYSKGVNRKLGKTGLYPSYKVREKIETVKYP--TYPEAE
                                                                                                                                                                      015471, 014963,
15-UTL-1998 (Rel. 36, Created)
15-UTL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Synaptonemal complex protein 1 (SCP-1 protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Testis;
MEDLINE=97224467; PubMed=9119375;
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                                                                                                                                                      STANDARD;
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SCP1 HUMAN
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99 NYKKQARNDLGKDHEILRRRIENGAKELWFFLQSELKKLKKLEGNELQRHADEILLDLGH 158
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                                           (POTENTIAL) . (POTENTIAL) . (POTENTIAL) .
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ASP/GLU-RICH (ACIDIC)
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LTSHCNKLSLENK -> YF7
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K -> T (IN REF. 2).
E -> D (IN REF. 2).
E -> D (IN REF. 2).
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last annotation update)
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01-APR-1993
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coiled coil; Repeat; Alternative splicing
                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: SEEMS TO BE A INTERMEDIATE FILAMENT ASSOCIATED PROTEIN THAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P30622-2; Sequence=VSP_000765;
--- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE REED-STERNBERG CELLS
OF HODGKIN'S DISEASE:
---- SIMILARITY: Contains 2 CAP-Gly domains.
                                                                                                                                TISSUE=Peripheral blood monocytes;
MEDLINE=92289675; PubMed=1600942;
Mablibe G., Delabie J., Brueggen J., Richener H., Asselbergs F.A.M.,
Cerletti N., Sorg C., Odink K., Tarcsay L., Wiesendanger W.,
de Wolf-Peeters C., Shipman R.;
"Restin: a novel intermediate filament-associated protein highly
expressed in the Reed-Sternberg cells of Hodgkin's disease.";
EMBO J. 11:2103-2113(1992).
                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
protein-170 alpha-2) (CLIP-170) (Reed-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=VSP 000765.
D -> E (\overline{IN} REF. 2).
W; 0A4F166DD94254E8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G0:0005882; C:intermediate filament; TAS.
G0:0015630; C:microtubule cytoskeleton; TAS.
G0:0008017; F:microtubule binding activity; TAS.
G0:0006899; P:non-selective vesicle transport; TAS.
                                                                                                                                                                                                                                                                                 MEDLINE=92405160; PubMed=1356075;
Pierre P., Scheel J., Rickard J.E., Kreis T.E.;
"CLIP-170 links endocytic vesicles to microtubules.";
Cell 70:887-900(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COILED COIL (POTENTIAL)
                filament associated protein)
                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Long;
IsoId=P30622-1; Sequence=Displayed;
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SER-RICH.
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InterPro; IPR000938; ZAF_CCHC.
Ffam; PP01302; CAP_GLY; Z.
SMART; SM00343; ZAF_CCHC; 1.
SMOSITE; PS00845; CAP_GLY 1; 2.
PROSITE; PS50245; CAP_GLY 2; 2.
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1427 AA; 160989
 (Cytoplasmic linker
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Genew, HGNC:10461; RSN.
                Sternberg intermediate
                                            (Human)
                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       CYTOSKELETON.
                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Short;
                                               sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420 KYSNYEFIS---DNSISWSAGLHNRY-----TENSLR-----GVILDIHFL-S 458
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                                                                                                                                                                                                                                                                                                       -----NELQRHADEILLDLGHHERSIMTDL
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                                                                                                  -----RRMAESLRIPEGPIDQGTATGRVR
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                                                 Indels 219;
Length 1427;
                       Best Local Similarity 17.9%; Pred. No. 4.7;
Matches 117; Conservative 104; Mismatches 215;
     DB 1;
  3.8%; Score 118.5; 17.9%; Pred. No. 4.7
                                                                                                  40 SRELSKILAKLERLKQQNEDL----
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1124 EELNKSKELLTVE-----
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     Query Match
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Search completed: February 2, 2004, 08:40:18 Job time : 14.5 secs Q8ir54 drosophila

5 QBIR54

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122
17
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1 MRAWIGSWRWIMLILFAWGT......XKVREKIETVKXPTYPEAEK 575
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Q8axs7 xenopus lae
Q8nep2 homo sapien
Q9vy5 d putative
Q9vy5 d putative
Q8iua5 homo sapien
Q8itw9 ciona intes
Q8ifw9 ciona intes
Q8isa7 leptospira
Q9ea5 plasmodium
Q9ea5 arabidopsis
Q9ea5 arabidopsis
Q9ea5 mono sapien
Q4812 homo sapien
Q8bu18 mus musculu Description QBAXS7 QBNEP2 Q9VVV5 O16882 QB1UA5 QB1FW9 QB1FW9 QB73E7 QBTX14 QBTX14 QBTX12 QB1ED2 QB1ED2 QB1ED2 QB1ED2 QB1ED2 QB1ED2 5 116 117 110 Query Match Length DB 446 619 559 169 1137 1137 876 1218 1218 681 1285 1285 681 1200 26.3 19.9 19.9 19.9 19.9

2783.5 2176 1489.5 991

810 671

614.5 137.5 132.5 128.1 127.5 124.1 124.1 122.5

014812 Q8BU18 Q921B9

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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2003 (TrEMBLrel. 23,
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                                                       QRTLILESQSWRYATGGWETVFKPVSETCTDRSGSSTGHWAGEANDKNVQVVELPIVDSL
                                                                                                                                                                                                      HPRPPYLPLGVPEDLADQLIRLHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLAFKH
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Strauberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ECO25385; A4412385.1; -.
InterPro; IPR001452; SH3.
SWART; SW00326, SH3; 1.
Hypothetical protein.
SEQUENCE 446 AA; 51138 MW; 89DAC51B0B7C57FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYSKGVNRKLGKTGLYPSYKVREKIETVKYPTYPEAEK 575
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYSKGINRKLGRTGLYPSYKVKEKIETVKYPTYQEAEK
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01-MAR-2003 (TrEMBLrel.
Hypothetical protein.
Homo sapiens (Human).
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01-OCT-2002 (TrEMBLrel.
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nes 398; Conserv
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REDLINE=20196006; PubMed=10731132;

RADAMS M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

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RAGONGE R.A., Lewis S.E., Richards S., Champe M., Pfeiffer B.D.,

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RADORO K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

Burtis R.J., Farangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RADORO K., Obup L.B., Gorrell J.H., Gu Z., Guan P., Harris M.,

RADORO K., Addira C.D., Kraft C., Kravitz S., Kull D., Lai Z.,

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RADAMS B.E., Kodira C.D., Kraft C., Kravitz S., Kull D., Mortis D.,

RADAMS B.E., Kodira C.D., Kraft C., Kravitz S., Kull D., Mortis C.,

RADAMS B.E., Kodira C.D., Kraft C., Kravitz S., Kull D., Mortis C.,

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RADAMS B.E., Kodira C.D., Kraft C., Kravitz S., Kull D., Mortis C.,

RADAMS B.E., Kodira C.D., Kraft C., Kravitz S., Kull D., Rogesse M.G.,

RADAMS B.E., Kodira C.D., Kraft C., Kravitz S., Kull D., Rogesse M.
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DFLVCTFSSQVCRVAYEIMQTLHPDASANFHSLDDIYYFGGQNAHNQIAVYPHQPRTKEE
                                                                                                                                                                                                                                                                                                              575
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Drosophila: characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative alpha-(1,6)-fucosyltransferase (EC 2.4.1.68) (Glycoprotein
                                                                                                                                                                                                                                                                                                                                                             392 IPMEPGDIIGVAGNHWDGYSKGVNRKLGRTGLYPSYKVREKIETVKYPTYPEAEK
                                                                                                                                                                                                                                                                                                              521 IPMEPGDIIGVAGNHWNGYSKGVNRKLGKTGLYPSYKVREKIETVKYPTYPEAEK
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Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Pshydroidea; Drosophilidae; Drosophila.
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"Core al. and a6-fucosyltransferases in Drosophila: char
and origin of diversity";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  619 AA
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GHASADLEBSINQVLLQGAEHKRSLLSDMERNRQSDGYEAWRHKEARDLSDLVQRRLHHL
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Science 282:2012-2018(1998).
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Submitted (DEC-2002)
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                                                                                                                                                                                                                                   Hypothetical protein, Transferase; Glycosyltransferase, Transmembrane; Signal-anchor; Golgi stack; SH3 domain.

DOMAIN

17 CYTOPLASMIC (POTENTIAL).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.W., Zhou W., Zhu S., Zhu X., Smith H.O. Gibbs R.A., Myers E.M., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49; Gaps
                                                                                              STRAIN=Berkeley; TISSUE=Testis;
Staplicon M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorset V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Munco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                     GLUCOSAMINYL) ASPARAGINE.
-!- PATHWAY: GLYCOSYLATION.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 619;
                                                                                                                                                                                                    PubMed=11698403;
Roos C., Kolmer M., Mattila P., Renkonen R.;
"Composition of Drosophila melanogaster proteome involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LUMENAL, CATALYTIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 48.3%; Score 1489.5; DB 5; Length Best Local Similarity 46.6%; Pred. No. 5e-99; Matches 285; Conservative 110; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            691BFD9B5C6557DE CRC64;
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                                                                                                                                                                   FRPVSETCTDRSGLSTGHWSGEVKDKNVQVVELPIVDSLHPRPPYLPLAVPEDLADRLLR
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Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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Martinez-Duncker I., Mollicone R.;
"Cloning, expression and genomic organization of two core
fucosyltransferases (CeE and CeD) from Caenorhabditis elegans.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF022968; AAN84870.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (10F3.6 (Core alpha-6-fucosyltransferase)
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Davidson S., Wohldmann P.;
"The sequence of C. elegans cosmid C10F3.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
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169
                               Transferase.
                                                                                                                         Best Local Sim
Matches 148;
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                                                    SEQUENCE
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                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 TDLYYLSQTDGAGEWREKEAKDLTELVQRRITYLQNPKDCSKARKLVCNINKGCGYGCQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 VKDKNVQVVELPIVDSLHPRPPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399 VDKKRVYLATDDPSLLKEAKTKYSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLS
                                                                                                                                               Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDINE=22326102; PubMed=12438718;

COULLIN P., Crooijmans R.P.M.A., Groenen M.A.M., Heilig R.,

Mollicone R., Oriol R., Candelier J.J.;

"Assignment of FUTS gene to chicken chromosome band 5q1.4 and to chromosome 14q23.2-24.1 by in situ hybridization. Conserved and cycopared synteny between human and chicken.";

Cytogenet. Genome Res. 97:234-238 (2002).

EMBL; AJ514324; CAD55804.1;
                                                                                                                                               64;
                                                                                                 Length 559;
                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                     MAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIENYKKQARND-
                               al protein; Glycosyltransferase; Transferase
559 AA; 63648 MW; BBF6F1944A9BEF9F CRC64;
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Last annotation update)
                                                                                                                                               Conservative 115; Mismatches 188;
                                                                                                 32.2%; Score 991; DB 5; 36.7%; Pred. No. 4.1e-63;
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(TrEMBLrel. 23, I
(TrEMBLrel. 23, I
EMBL; AJ512486; CAD54736.1;
Hypothetical protein; Glycos
SEQUENCE 559 AA; 63648 MW
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FUT8.
                                                                                                                       Best Local Similarity
Matches 213; Conserv
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57 ILEKER-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Michalski J.C., Bauvy C., Cailleau-Thomas A.,
Mollicone R., Michalski J.C., Bauvy C., Cailleau-Thomas A.,
Mollicone R., Martinez-Duncker I., Breton C., Codogno P., Oriol R.,
Splice variants of alpha-6-fucosyltransferase are expressed early in
human embryogenesis.",
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ515151, CAD5616.11, -.
Transferase; Glycosyltransferase.

Transferase; Glycosyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 KDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQNWRYAT----GGWET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 VFRPVSETCTD-RSGLSTGHWSGEVKDKN-----VQVVELPIVDSLHPRPPYLPLAVPED
                                                                                                                                                                                           420 KYSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIM
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Rukaryota: Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
NCBI_TaxID=7719;
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                                                                                     26.3%; Score 810; DB 4; Length 169; llarity 94.9%; Pred. No. 9.2e-51; Conservative 5; Mismatches 3; Indels
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                                             19520 MW; 0ACD43AA0F56AB31 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative alpha-6-fucosyltransferase (EC 2.4.1.68).
                                                                                                                                                                                                                                                                                                                                                                                        540 SKGVNRKLGKTGLYPSYKVREKIETVKYPTYPEAEK 575
                                                                                                                                                                                                                                                                                                                                                                                                                  134 SKGVNRKLGRTGLYPSYKVREKIETVKYPTYPEAEK 169
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EMBL; AJ514325; CAD55805.1;
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Matches 157; Conservative
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21, Last sequence update)
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                 PRELIMINARY;
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es 95; Conserv
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LA2459.
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01-MAR-2003
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SEQUENCE FROM N.A.

Mollicone R., Michalski J.C., Bauvy C., Cailleau-Thomas A.,

Candelier J.J., Martinez-Duncker I., Breton C., Codogno P., Oriol R.;

Spiler variants of alpha-6-fucosyltransferase are expressed early in

human embryogenesis.";

Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ515152, CAD556162.1;

Transferase; Glycosyltransferase.

SEGOS MW, DEC70B7A0ECE6281 CRC64;
                        342 QOSTSHADTSSRLSSBGLKGIVTDVHLLVECDHFVGTFSSNIGRLVYEMKQQYGSDPTFT
                                                                                                             177 HYTICLFISLGTGRVMMSNMSNLAYP--NMDKIFLPLSRTCLTAEGNVDDYPEWESPNDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    456 FLSQADFLVCTFSSQVCRVAYEIMQTLHPDASANFHSLDDIYYFGGQ-----NAH--
                                                                                    ---RTKEEIPMEPGDII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 EVKDKAVQVVELPIVDSLHPRPPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 ETVVRRIFLATDDILIGSQLKITYPKYRIVQIQKNAV---VALAKRFSGSGLEGILQDVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.9%; Score 614.5; DB 5; Length 560; 28.4%; Pred. No. 6e-36;
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                                                                                                                                                                       530 GVAGNHWNGY-SKGVNRKLGKTGLYPSYKVREKIETVKYPTY 570
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Bukaryota, Metazoa; Chordata; Uro
Phlebobranchia; Cionidae; Ciona.
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Last sequence update)
Last annotation update)
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llarity 20.9%; Pred. No. 0.41;
Conservative 96; Mismatches 155;
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SEQUENCE FROM N.A.

STRAIN=AV19 / DSM 6324 / JCM 9639;

MEDLINE=21927647; Pubmed=11930118;

Slegarev A.I., Mazhevaya K.S., Polushin N.N.,

A Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,

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RITERPRO; IPR003499; ABC_transporter.

RITERPRO; IPR003499; ABC_transporter.

RITERPRO; IPR003499; SWC_N.

RITERPRO; IPR002017; Spectrin.

R Pfam; PF02463; SWC_C; 1.

RR Pfam; PF02463; SWC_C; 1.
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Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
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llarity 19.5%; Pred. No. 0.98;
Conservative 82; Mismatches 186; Indels 108; Gaps
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Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 674 AA; 76676 MW; CF26CDFE4B9CF8DC CRC64;
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Last sequence update)
Last annotation update)
674 AA
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PRT;
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MEDLINE-99069613; PubMed-9851916;
                                             01-NOV-1996 (TrEMBLrel. 01, Crt 01-OCT-2001 (TrEMBLrel. 18, Las 01-MAR-2003 (TrEMBLrel. 23, Las Hypothetical 76.7 kDa protein. C18H9.8.
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EMBL; U23147; AAC46692.2; -.
HSSP; P04268; 1IC2.
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Science 282:2012-2018(1998).
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PRELIMINARY;
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Favello A., Favello T.;
"The sequence of C. eleg
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Submitted (MA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٦,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | : ::|:| :||:| :||:| | :|| | | :::|| | ITELQSSFSSYENEMRHVVKKIE--DLEKKKSENILDLKKLENTLL-DLQKDLKTSSDTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Li J., Lee J.M., Kremenetskaia I., Luros J., Ngan I., Liu A.,
Gonzalez A., Altafi H., Araujo R., Chao Q., Conn L., Conway A.B.,
Dunn P., Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn P.,
Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
                                                                                                                                                                                                                                                                                                                                                                                                                     Harris B., Lennard N., Clark L., Line A., Barron A., Corton C., Harris B., Lennard N., Clark L., Line A., Chillingworth C., Doggett Bertiman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AL844509; CAD52328.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1218;
                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Chromosome segregation protein, putative.
MAL13Pl.96
Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI TAXID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 AKEL---WFFLQSELKK-LKKLEGNELQRHADEILLDLGHHERSIMTDLY
                                  626 AVEKRTAAKSLDMSLRKTE----IDYEDIKTESIRLQEEYNNMLLTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
399 VDKKRVYLATDDPSLLKEAKTKYSNYEFISDNSISWSAGLHNRYTEN
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.1%; Score 127.5; D 24.8%; Pred. No. 2.4;
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01-MAY-2000 (TrEMBLrel. 13, Last sequenc
01-DEC-2001 (TrEMBLrel. 19, Last annotat
F25C20.13 protein.
F25C20.13.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                 Created)
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NR 1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 KDHEIL----RRR(ENGAKELWF--FLOSELKKLKKLEGNELQRHADE-----ILLD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----AYMMDFVFSEKEDG-GIFDNKNGLDYHLPVVGGISKEPPLHIVHIAVEMAPIAK 591
                                                                                                                                                                                                                                                                                                                                                                                         26
                                                                                                                                                                                                                                                                                                                                                                                                                            SGNW-WFAEVVVPGGALVIDWVFADGPPKGAFLYDNNGYQDFHALVPQKLPEBLYWLEEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 TGSWRWIMLILFAWGTLLF-YI-----GGHLVRDNDHPDHSSRELSKILAKLERLKQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEDLRRMAESLR: PEGPI -----DQGTATGRVRVLEEQLVKAKEQIENYKKQARNDLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   592 VGGLGDVVTSLSKAVQELNHNVDIVFPKYDCIKHNFVKDLQFNRSYHWGGTEIKVWHGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               652 EGLSVYFLDPQN(3LFQRGCVYGCADDAGRFGFFCHAALEFLLQGGFHPD-ILHCHDWSSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 WLEREI-----EETTKKLGFK---HPVIGVHVRRIDKVGTEAAFHPIEEYMVHVBEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         802 YISENVVEGKRANKEELONRLGLKSADFPVVGIITRLTHQKG-------IHLIKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----INKGCGYGCQ----LHHVVYCFMIAYGTQRTLILESQNWRYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 TGGWETVFRPVSHTCTDRSGLSTGHWS--GEVKDKNVQVVELPIVDSLH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        747 AMTFADKATTVSPTYAKEVAGNSVISAHLYKFHGIINGIDPDIWDPYNDNFI----PVP
                                                                                                                                                                                                                                                                                                                                       Gaps
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NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                          4.0%; Score 124; DB 10; Length 1025; 18.6%; Pred. No. 3.4; trive 79; Mismatches 184; Indels 240;
"Arabidopsis thaliana chromosome 1 BAC F25C20 sequence.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                               EMBL; AC007296; AAD30251.1; -.
SEQUENCE 1025 AA; 116411 MW; 08C952A2032BA1E4 CRC64;
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                                                                                                                                                               to the EMBL/GenBank/DDBJ databases
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1-MAY-2000 (TrEMBLrei. 13, Last sequence update)
01-OCT-2002 (TrEMBLrei. 22, Last annotation update)
Hypothetical protein KIAA0389.
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                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                    SEQUENCE FROM N.A. STRAIN=cv. Columbia;
                                                                                                                                                                     (MAY-1999)
                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 115; Conserv
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Genew; HGNC:1859; CEP2
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                        SEQUENCE
                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1154 QIPARQREIEMNRQQRFFRIPFIRPADQYKDPQSKKKGWWYAHF-----DGPWIARQME 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 069 ------LRDTINTSC 1093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 RKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQNWRYATGGWETVFRPVSETCT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 -----VPEDLADRLLRV-----HGDPAV----WWVSQFVKYLIRPQPWLEREIE 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Autoantibodies to a group of centrosomal proteins in human autoimmune sera reactive with the centrosome.";
Arthris Rheum. 41:551-558(1998).
EMBL; AF022655; AAC06349.1;
HSSP; P04268; 11C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : | | ::| | :||
1014 LRIAQSEAELISDEAQADLALRRNDGTRPKMTPEQMAKEMSEPLSRGPAVL----ATKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 LDLGHHERSIMTDL----YYLSQTDGAGE--WREKEAKDLTELVQRRITYLQNPKDCSKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 SSRELSKILAKLERLKQQNEDLRRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 D------RSGLSTGH-WSGEVKDKNVQ------VVELPIVDSLHPRPPYLPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                       Ohira M., Seki N., Miyajima N.,
                                                                                 Nagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N. Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. VI The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; DNA Res. 4:141-150(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
4.0%; Score 124; DB 4; Length 1285;
Best Local Similarity 20.3%; Pred. No. 4.6;
Matches 73; Conservative 51; Mismatches 128; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
BEDILNE-29165428; PubMed-9506584;
Mack G.J., Rees J., Sandblom O., Balczon R., Fritzler M.J.,
Rattner J.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1285 AA; 148713 MW; BCB4FDFE920712CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JNN-1998 (TrEMBLrel. 05, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 2442 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cep250 centrosome associated protein.
                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00612; IQ; 1.
Pfam; PF00063; myosin head; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                           MEDLINE=97349984; PubMed=9205841;
                                                                                                                                                                                                                                                                                            4SSP; PO8799; IMMD.
InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00015; IQ; 1.
SMART; SM00242; MYSc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 1285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         014812
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137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1148 KAAQLH-----LRLRSTESQLEALAAEQQPGNQAQAQLASLYSALQQALGSVCESRP 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1202 ELSGGGDSAPSVWGLEPDQNGAR----SLFKRGPLLTALSAEAVASALLKLHOD-- 1251
                                                                                                                                                                                   43 LSKILAKLERLKQQNEDLRRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIENYKK 102
                                                                                                                                                                                                                          138 KKLE----GNELQRHADEILLDLGHHERSIMT------DLYYLSQ--TDGAGEWR 180
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The FANTOM Gonome Exploration Research Group Phase I & II Team;
the RIKER Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBI; AKO88078; BAC40132.1; -.
NON TER 681 681
SEQÜENCE 681 AA; 78710 MW; 15D1F74CB48FB2EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 GLSTGH-----WSGEVKDKNVQVVELPIVDSLHPRPPYLPLAVPEDLADRLLRVHGDPA
                                                                                                                                                                                                                                                                                                                    OARNDLG-----KKL
                                                                                                                                                                                                                                                                                                                                                                                986 OHRDDLAALQEESSSLLQDKMDLQKQVED-----LKSQLVAQDDSQRLVEQEVQEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------KEAKDLTELVQRRITYLQNPKDCSKARKLVCNINKGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 YGCQLHHVVYCFMIAYGTQ----RTLILESQNWRYATGG-----WETVFRPVSETCTDRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 HVEEHFOLLERRMKVDKKRVYLATDDPSLLKEAKTKYSNYEFISDNSISWSAGLHNRYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325 VWWVSQFVKYLIRPQPWLEREIEETTKKLGFKHPVIGVHVRRTDKVGTEAAFHPIEEYMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.0%; Score 122.5; DB 11; Length 681;
llarity 21.1%; Pred. No. 2.5;
Conservative 62; Mismatches 207; Indels 139; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                     *Match 4.0%; Score 124; DB 4; Length 2442; Local Similarity 19.6%; Pred. No. 11; les 96; Conservative 76; Mismatches 139; Indels 180;
2442 AA; 281000 MW; B66458A0BF308C24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Nuclear pore complex-associated protein TPR (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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1252 -LWKTQQTRDVLRDQ---VQKLEE-
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SEQUENCE FROM N.A.
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Matches 109;
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3 FYIGGHLVRDNDHPDHSSRELSKILAKLERLKOQNEDLRRMAESLRIPEGPIDQGTATGR 82	3 VRVLEBOLVKAKEQIENYKKQARNDLGKDHEILRRRIENGAKELWFFLQSELKKLKKL 140	106 NLGIQSQFTRAKEELEAEKRDLIRTNERLSQEVEYLTEDVKRLNEKLK 153	EGNELQRHADEILLDLGHHERSIMT	4 BSNTTKGELQLKLDELQASDVAVKYREKRLEQEKELLHNQNS 195	7 YLQNPKDCSKARKLVCNINKGCGYGCQLHHVVYCPMIAYGTQRTLILESQNWRYATG 253	6 WINTELKTYTDELLALGREKGNEILELKCNLENKKEEVLRLEEGWNGLKTS 246	4 GWETVFRPVSETCTDRSGLSTGHWSGEVKDKNVQVVELPIVDSLHPRPPYLPL 306	7 N-EHLOKGIVEDLITYKIKBAKEQQASMEEKFHNELNAHIKLSNLYKSAADDSEAKSNELTR 305	7 AVPE	6 AVDELHKLLKEAGEANKTIODHLLQVEESKDQMEKEMLEKIGKLEKELENANDIL 360	4 GFKHPVIGVHVRRIDKVGTEAAFHPIBEYMVHVEEHFQLLER 395	1 SATKRKGAILSEBELAAMSPTAAAVAKIVKPGMKLTBLYNAYVETQDQLLLE 412	6 RMKVDKKRVYLATDDPSLLKEAKTKYSNYEFISDNSISWSAGLHNRYTENSLRGVILDIH 455	3KQENKRINKYLDEIVKEVEAKAPILKRQREE 443	6 FLSQADFLVCTFSSQVCRVAYEIMQTLHPDASANFHS 492	444 -YERAQKAVASLSAKLEQAMKEİQRLQEDTDKANKHS 479	
23 F 55 F	83 V	106 N	141 B	154 B	197 Y	196 W	254 G	247 N	307 A	306 A	354 G	361 S	396 R	413 -	456 F	444 -	
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Search completed: February 2, 2004, 08:43:08 Job time : 37.5 secs THIS PAGE BLANK (USPTO)

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; Search time 38.5 Seconds
(without alignments)
2370.592 Million cell updates/sec
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3085
1 MRAWIGSWRWIMLILFAWGT......YKVREKIETVKYPTYPEAEK 575
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- /SIDS17gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:
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/SIDS1/gcgdata/geneseq/genesegp-embl/AA1988.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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/SIDS1/gcgdata/geneseq/geneseqp-embl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1107863 segs, 158726573 residues
                                                                                                                                                                          February 2, 2004, 08:39:39
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Antibody productio	Antibody productio	Human alpha 1-6 fu	Alpha1,6-fucosyl t	Pig alpha 1-6 fuco	Human colon cancer	Human alpha 1-6 fu	Drosophila melanog	Human alpha 1-6 fu
SUMMARIES	ΩI		ABG34135	AAW22125	ABB08405	AAW22124	AAG73884	AAB75061	ABB59117	AAB75062
	DB	23	23	18	23	18	22	22	22	22
	Length	575	575	575	575	575	515	339	619	233
de	Query e Match Length DB I	100.0	98.0	97.3	97.3	94.3	86.2	57.6	48.0	39.1
	Score	3085	3024	3003	3003	2910	2658	1778	1480.5	1206
	Result No.	1	7	m	4	2	9	7	80	6

WPI; 2002-340182/37

## ALIGNMENTS

RESULT 1

Antibody production; cytostatic; immunomodulator; vasotropic; virucide; antibacterial; antiinflammatory; antiallergic; allergy; inflammation; autoimmune disease; Chinese hamster ovarian tissue-originated cell; CHO; tumour; circulatory disease; infection. Yamane N; Shinkawa T, Antibody production method related protein #1. Nakamura K, Uchida K, , Yamasaki M, Hanai N; ABG34136 standard; Protein; 575 AA (KYOW ) KYOWA HAKKO KCGYO KK. 05-OCT-2001; 2001WO-JF08804. 06-OCT-2000; 2000JP-0308526. 15-JUL-2002 (first entry) Yamano K, Satoh M, WO200231140-A1. Mus musculus. 18-APR-2002. Kanda Y, ; Hosaka E, ABG34136; 

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                                                                                                                                                                                         This invention relates to novel method for antibody production comprising a Chinese hamster ovarian tissue-originated (CHO) cell transferred with a gene encoding an antibody molecule for producing a composition comprising an antibody molecule with an Fc domain bonded to the N-glycoside linkage complex sugar chain. The produced antibody compositions are drugs for prevention or treatment of diseases accompositions are drugs for prevention or treatment of diseases, circulatory diseases, and viral and bacterial infections. The antibodies can be stably produced using the method of the invention with high binding activity and potency thus leading to high safety and treduced side effects when applied alone or in combination with other drugs for therapy. The present sequence represents a protein molecule used in the method of the invention.
Cells producing antibody compositions including antibody fragments and fusion proteins with Fc domain of antibody, useful for prevention or treatment of cancer, immune diseases, circulatory diseases and
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; Pred. No. 3.1e-279;
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Best Local Similarity 100.0%;
Matches 575; Conservative 0
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Pred. No. 1.6e-273,
9; Mismatches 5,
                                                Antibody production method related protein #1
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Yamasaki M, Hanai N;
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               15-JUL-2002 (first entry)
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Yamano K,
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            PPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVI 360
                        PPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLERBIBETTKKLGFKHPVI
                                                                YSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIMQ
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diphosphate; sugar chain synthesis; modification; antibody;
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                                                                                                                                                                                                                                                                                                                      Human alpha 1-6 fucosyltransferase.
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96JP-0161648.
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                                                                                                                                                                                                                                                                                                                                                       guanosine diphosphate; su
GlcNAc; cancer diagnosis.
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enzyme is useful in the synthesis and
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    in the presence of 5 mM EDTA. The enzyme is useful in the synthesis modification of sugar chains, and as antigen for the production of antibodies recognising the enzyme. The antibodies can be used for diagnosis of cancer and other diseases.
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                                                                                                                                                               97.3%; Score 3003; DB 18; Length 575; 96.5%; Pred. No. 1.4e-271;
                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                         11; Mismatches
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Matches 555; Conservative
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AAW22124 standard; Protein; 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                         The invention relates to a plant cell with an animal type sugar chain adding function, created by transforming a tobacco cell with a gene encoding an enzyme derived from an animal which can transfer a fucose residue to the reductive end acetylglucosamine residue of a sugar chain. The gene that is introduced into the plant cell encodes the enzyme apphal, 6-tucosyl transferase. The method of the invention is useful for the preparation of a glycoprotein having animal type sugar chain. The current sequence represents alphal, 6-fucosyl transferase amino acid
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                                                                                                                                   A plant cell with an animal type sugar chain adding function, preparation of a glycoprotein with an animal type sugar chain
                                                                                                                                                                                                                                                                                                                                                                                               Length 575;
                                                                                                                                                                                                                                                                                                                                                                                               97.3%; Score 3003; DB 23; 96.5%; Pred. No. 1.4e-271;
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Matches 555; Conservative 11; Mismatches
                                                                                                                                                                                 Example 1; Page 24-26; 38pp; Japanese
22-MAR-2000; 2000JP-0081059
                             TANIGUCHI N.
                                                                                       WPI; 2002-158816/21
N-PSDB; ABA98809.
                                                           FUJIYAMA K.
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Lucosyltranaferases of the invention, respectively. The enzyme transfers fucosyltranaferases of the invention, respectively. The enzyme transfers fucosyltranaferases of the invention, respectively. The enzyme transfers fucosyltranaferases of the invention for the GloNAcoverse from guanosine diphosphate to the 6-hydroxyl group of the GloNAcoverse to R in the receptor molecule: (GloNAcovera 1-2Manalpha 1-6) (GloNAcovera 1-4GloNAcovera 1-4GloNAcover to give (GloNAcovera 1-2Manalpha 1-6) (GloNAcovera 1-3) Manbeta 1-4GloNAcovera 1-3 Manbeta 1-4GloNAcovera 1-3 Manbeta 1-4GloNAcovera 1-3 Manbeta 1-4GloNAcovera 1-4 Manalpha 1-6) (GloNAcovera 1-3) Manbeta 1-4GloNAcovera 1-4 Manalpha 1-6 Manaly, and is stable over the PH range 4-10 after 5 hours at 4 degrees C. The optimum working temperature of the 1-10 after 5 hours at 4 degrees C. The optimum working temperature of the 1-10 after 5 hours at 4 degrees C. The optimum working temperature of the 1-10 after 5 hours at 1-6 modification of segar chains, and as antigen for the production of antibodies recognising the enzyme. The antibodies can be used for the antibodies can be used for the diagnosis of cancer and other diseases.
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                                                                                                       Alpha 1-6 fucosyltransferase; enzyme; pig; human; fucose transfer; guanosine diphosphate; sugar chain synthesis; modification; antibody; GlcNAc; cancer diagnosis.
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used as an antigen
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                                               Pig alpha 1-6 fucosyltransferase.
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96JP-0010365.
96JP-0161648.
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(first entry)
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24-JAN-1996;
21-JUN-1996;
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05-MAR-1998
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RESULT 5 AAW22124

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LALESHWWRYATGGWETVFRPVSETCTDRSGSSTGHWSGEVKDKWVQVVELPIVDSVHPR
                                                                                                                    ALHPDASANFRSLDDIYYFGGPNAHNQIAIYPHQPRTEGEIPMEPGDIIGVAGNHWDGYP
                                                                    PPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVI
                                                                              PPYLPLAVPEDLADRLVRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVI
                                                                                                          GVHVRRTDKVGTEAAFHPIEEYMVHVEEHFQLLARRMQVDKKRVYLATDDPTLLKEAKTK
                                                                                                                                                YSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIMQ
                                                                                                                                                           YPSYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIMQ
                                                                                                                                                                                      TLHPDASANFHSLDDIYYFGGQNAHNQIAVYPHKPRTEEEIPMEPGDIIGVAGNHWDGYS
                                                                                                                                                                                                                                                                                                                                                                            colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                         Human colon cancer antigen protein SEQ ID NO:4648
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99US-0163280
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N-PSDB; AAH33315.
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03-NOV-1999;
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inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the mucleic acids into a host cell and culturing the cell co express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH77196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 SQNWRYATGGWEÏVFRPVSETCTDRSGISTGHWSGEVKDKNVQVVELPIVDSLHPRPPYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTDKVGTEAAFIPIEEYWVHVEEHFQLLARRMQVDKKRVYLATDDPSLLKEAKTKYPNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S KSLRIPEGPIDQ;PAIGRVRVLEEQLVKAKEQIENYKKQTRNGLGKDHEILRRRIENGAK
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                                                                                                                                                                                                            for
                                                                                                                                                            present invention.

NB. Pages 66 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
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                                                                                                                                                                                                                                                                                                                                         515;
                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                      Score 2658; DB 22;
Pred. No. 2.2e-239;
2; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                         36.2%;
96.1%;
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Best Local Similarity 96.18
Matches 491; Conservative
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                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                       The present invention describes an anti-human alpha 1-6 fucose fucosyltransferase (alpha 1-6 fucT, also called alpha 1-6 fucose transferase) antibody. Also described are: (1) a hybridoma producing the above monoclonal antibody; (2) an immunoassay for detecting human alpha 1-6 fucT by using the above antibody or its antibody fragment; and (3) a reagent used for the above immunoassay. The anti-human alpha 1-6 fucT antibody can be used for immunoassay. The present sequence represents the human alpha 1-6 fucT protein of residues 237 to 575, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                            121 HPVIGVHVRRIDKVGTEAAFHPIEEYMVHVEEHFQLLARRMQVDKKRVYLAIDDPSLLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                           237 TORTLILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVNDKNIQVVELPIVDS
                                                                                                                                                                                                                                                                                                                    1 TQRTLILESQNWRYATGGWETVFRPVSETCTDRSGISTGHWSGEVKDKNVQVVELPIVDS
                                                                                                                                                                                                                                                                                                                                                 297 LHPRPPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFK
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                                                                                                                                                                                                                                                                 Length 339;
                                                                                         Novel anti-human alphal-6 fucose transferase antibody useful
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                                                                                                                                                                                                                                                                 57.6%; Score 1778; DB 22; 96.2%; Pred. No. 2.3e-157;
                                                                                                                                                                                                                                                                                      9; Mismatches
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                                                                                                                      Example 2; Page 8-9; 11pp; Japanese
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                    99JP-0183569
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                                       (FJRE ) FUJIREBIO KK
                                                          WPI; 2001-275926/29.
N-PSDB; AAF87952.
                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                              339 AA;
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29-JUN-1999;
                    29-JUN-1999;
                                                                                                    immunoassay
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258 VFRPVSETCTDRSGLSTGHWSGEVNDKNIQVVELPIVDSLHPRPPYLPLAVPEDLADRLL 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -HLEGNELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGDWREKEAKDLTELVQRRITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVIGVHVRRTDKVGTEAAFH
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::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | ::|| | 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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 4143; 21pp + Sequence Listing; English
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Best Local Similarity 46.5%; Pred. No. 4e-129,
Matches 285; Conservative 108; Mismatches 16
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11-JUL-2000; 2000US-0614150.
23-MAR-2001; 2001WO-US09231
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197 246 257

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363 377 423 437

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes an anti-human alpha 1-6 fucose fucosyltransferase (alpha 1-6 fucr, also called alpha 1-6 fucose transferase) antibody. Also described are: (1) a hybridoma producing the above monoclonal antibody; (2) an immunoassay for detecting human alpha 1-6 fucr by using the above antibody or its antibody fragment; and (3) a reagent used for the above immunoassay. The anti-human alpha 1-6 fucr antibody can be used for immunoassay. The present sequence represents the human alpha 1-6 fucr protein of residues 343 to 575, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVCTFSSQVCRVAYEIMQTLHPDASANFHSLDDIYYFGGQNAHNQIAVYPHKPRTEEEIP
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                                                                                                                                                                                                               Human, alpha 1-6 fucosyltransferase, alpha 1-6 fucT, antibody; alpha 1-6 fucose transferase; anti-human alpha 1-6 fucT; immunoassay.
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                                                                                                                                                                                            Human alpha 1-6 fucosyltransferase protein 343-575 SEQ ID NO:4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 9-10; 11pp; Japanese.
                                                                                                                          AAB75062 standard; Protein; 233 AA.
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604 VEEKVDTAKLPLY 616
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                                             558 VREKIETVKYPTY
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                                                                                                                AAB75062
                                                                                                     RESULT
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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes cidentified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention.

Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                           Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia,
hypercholesterolaemia, coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver
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                                                                                                                                                                                    SEQ ID No 27452.
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ABG48804 standard; Peptide; 82 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-2000; 2000US-0:07456.
30-JUN-2000; 2000US-0:08408.
03-AUG-2000; 2000US-0:3266.
21-SEP-2000; 2000US-0:34687.
27-SEP-2000; 2000US-0:36879.
04-OCT-2000; 2000GB-0:024263.
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                                                                                                                    (first entry)
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Matches 79; Conserv
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                                                                                                                                                                                    Human liver
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                                                          ABG48804;
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ABB28797

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280 EVNDKNIQVVELPIVDSLHPRPPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQ 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                        Peptide #1491 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID NO 26620; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.0%; Score 432; DB 22; Length 82; 96.3%; Pred. No. 2e-32; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W, Rank DR;
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                                                             ABB33985 standard; Peptide; 82 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB19422 standard; Protein; 82 AA.
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2000US-0207456.
2000US-0608408.
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 AA;
                                                                                                                                                                                                                                                                                                                                                     WO200157277-A2.
                                                                                                                                                           04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000;
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                                                                                                               ABB33985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical egents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 EVNDKNIQVVELPIVDSLHPRPPYLPIAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQ 339
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                                                                                                                                        Peptide #1448 encoded by breast cell single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from humar breast, comprises number of single exon nucleic acid probes
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                                                                                                                                                                                         Human; microarray; single exon probe; gene expression; breast;
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ABB28797 standard; Peptide; 82 AA.
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26-WAY-2000; 2000US-0207456.
30-UMA-2000; 2000US-0608408.
31-34UG-2000; 2000US-0532366.
21-SEP-2000; 2000US-0234687.
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                                                                                           (first entry)
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hes 79; Conservative
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                                                                                                                                                                                                                    disease; cancer.
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                                              ABB28797;
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Query Match

Best Loca Matches

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microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 AA;
                  epilepsy; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157276-A2.
                                                                               WO200157275-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                  Protein #1421 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single exon nucleic acid probes for analyzing gene expression in human hearts -
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                                               gene expression; heart; microarray; vascular system; vascular disease; hypertension; cardiac arrhythmia;
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Best Local Similarity 96.3%;
Matches 79; Conservative
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2000US-0608408.
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2000US-0236359
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                                                                             congenital heart disease.
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                                                                                                                                              WO200157274-A2
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27-SEP-2000;
                                                                                                                Homo sapiens
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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                              Single exon nucleic abid probes for analyzing gene expression in human
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Pred. No. 2e-32;
2; Mismatches
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                                            2000US-0180312.
2000US-0207456.
2000US-0508408.
2000US-0532366.
2000US-0234687.
30-JAN-2001; 2001WO-US00667.
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Best Local Similarity 96.5.
To 79; Conservative
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XX
26-MAY-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0608408.
PR 30-JUN-2000; 2000US-0608408.
PR 30-JUN-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-023466.
PR 21-SEP-2000; 2000US-023466.
PR 27-SEP-2000; 2000US-023456.
PR 27-SEP-2000; 2000US-02346.
PR 27-SEP-2000; 2000US-02346
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340 PWLEKEIEEATKKLGFKHPVIG 361

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61 PWLEKEIEEATKKLGFKHPVIG

Query Match 14.0%; Score 432; DB 22; Length 82; Best Local Similarity 96.3%; Pred. No. 2e-32; Matches 79; Conservative 2; Mismatches 1; Indels

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Sequence 10, Appl
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-442-629-10
US-09-913-805A-2
US-09-442-629-12
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US-09-442-629-12
US-08-913-805A-12
US-09-142-629-12
US-09-144-629-13
US-09-144-629-3
US-08-913-805A-3
US-08-913-805A-3
US-08-913-805A-3
US-08-913-805A-3
US-08-913-805A-1056
US-08-198-452A-1056
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-09-606-304-12
-09-107-532A-3910
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                                                                                                                                                                                                                               328717 seqs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
                                                   - protein search, using sw model
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Maximum DB seq length: 2000000000
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Sequence 2, App Sequence 3, App Sequence 13, 7, Sequence 2, App Sequence 6, App Sequence 7, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 12, App Sequence 13, App Sequence 3, App Sequence 3, App Sequence 3, App Sequence 2, App Sequence 3, App Sequence 2, App Sequence 2, App Sequence 2, App		
28 101 3.3 2185 2 US-08-822-445-2 29 101 3.3 2185 4 US-09-396-540-2 30 100 3.2 3818 4 US-09-396-540-2 31 100 3.2 3818 4 US-09-914-259-11 32 99.5 3.2 97.4 4 US-09-914-259-11 34 99.5 3.2 97.5 4 US-09-914-259-67 35 99.5 3.2 97.5 4 US-09-750-580-3 36 99 3.2 1077 4 US-09-750-580-3 38 99 3.2 1077 4 US-09-750-580-3 39 3.2 1005 2 US-08-935-460-4 39 3.2 1005 2 US-08-935-07261-11 39 97.5 3.2 1663 5 PCT-US93-07261-11 41 97.5 3.2 1663 6 US-09-575-101-3 42 97.5 3.2 1647 4 US-09-535-008-7 45 97.5 3.2 1647 4 US-09-535-008-7 45 97.5 3.2 1647 4 US-09-535-008-7	ALIGNMENTS	RESULT 1  US-08-91-805A-10  Sequence 10, Application US/08913805A  Fatent No. 605430  APPLICANT: TANIGUGHI, Nactumi APPLICANT: TANIGUGHI, Nactumi APPLICANT: TANIGUGHI, Nactumi APPLICANT: SHIBA, Tetsuo APPLICANT: SHIBA, Tetsuo APPLICANT: SHIBA, Tetsuo APPLICANT: SHIBA, Tetsuo APPLICANT: TANIGUGHI, Nactumi APPLICANT: SHIBA, Tetsuo APPLICANT: TANIGUGHI, Nactumi APPLICANT: ANDRESS: CORRESPONDENCES: 15 CORRESPONDENCES: 15 CORRESPONDENCE ADDRESS: 15 CORRESPONDENCE ADDRESS: 15 CORPUTER: DC COUNTRY: DC COUNTRY: DC COUNTRY: DC COUNTRY: SHAPICATION DATA: APPLICATION NUMBER: US/08/913,805A FILING DATE: 23 JAM1 1997 CORRESPONDENCE: 23 JAM1 1997 APPLICATION NUMBER: UP 192260 FILING DATE: 23 JAM1 1997 APPLICATION NUMBER: UP 19260 FILING DATE: 23 JAM1 1996 APPLICATION NUMBER: UP 162813 FILING DATE: 22 JAM1 1996 APPLICATION NUMBER: UP 10365 ATIONE DATE: 24 JAM 1996 ATIONE TELEPAN: COL-429-0796 ATIONE TELEPAN: COL-429-0

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FILING DATE: 23 JAN 1997
APPLICATION NUMBER: DF 19260
FILING DATE: 22 JUL 1996
APPLICATION NUMBER: JP 162813
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JAN 1996
ATTORNEY/AGENT INFORMATION:
NAME: TOFFENELLY, JOINTH, L.
REGISTRATION NUMBER: 39 048
REFERENCE/DOCKET NUMBER: 39 048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGINRKLGKTGLYPSYKVREKIETVKYPTYPEAEK
                                APPLICATION NUMBER: US/08/913,805A FILLING DATE: 7 JAN 1998
6291219-1999
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-442-629-10
                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 202-429-1776
                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO: 10:
18-No.
FILING DATE:
APPLICATION
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                                                                                                                                                                                             61 RRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIENYKKQARNGLGKDHEILRRRIE
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                                                                                                                                                                                                                                                                                     121 NGAKELWFFLQSELKKLKNLEGNELQRHADEFLLDLGCHERSIMTDLYYLSQIDGAGDWR
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UOZUMI, Naofumi
SHIBA, Tetsuo
XANAGIDANI, Shusaku
TITLE OF INVENTION: Alba 1-6 Fucosyltransferase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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o
                                                   Query Match 97.3%; Score 3003; DB 3; Best Local Similarity 96.5%; Pred. No. 4.5e-274; Matches 555; Conservative 11; Mismatches 9;
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STREET: 1025 Connecticut Avenue, N.W.,
CITY: Washington
STATE: DC
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3+ Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: Wordberfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/442,629
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Patent No. 6291219
GENERAL INFORMATION:
   peptide
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 MOLECULE TYPE:
     ; MOLECULE 115
US-08-913-805A-10
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181 EKEAKDLTELVÇRRITYLQNPKDCSKAKKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRT 240
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                                              LILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVNDKNIQVVELPIVDSLHPR
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SHIBA, Tetsuo
YANAGIDALI, Shusaku
TITLE OF INVENTION: Alpha 1-6 Fucosyltransferase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541 KGINRKLGKTGLYPSYKVREKIETVKYPTYPEAEK 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: WordPerfect 6.1 Windows
SOFTWARE: WordPerfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/442,629
FILING DATE: 18 No. 6291219-1999
PRIOR APPLICATION NUMBER: US/08/913,805A
FILING DATE: 7 JAN 1998
APPLICATION NUMBER: PCT/UP97/00171
FILING DATE: 23 JAN 1997
APPLICATION NUMBER: JP 192260
FILING DATE: 23 UJU 1996
APPLICATION NUMBER: JP 162813
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 161848
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 10365
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REGISTRATION UNBER: 39,048
REPERENCE/DOCKET NUMBER: 2356/3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TANIGUCHI, Naoyuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2, Application US/09442629; Patent No. 6291219; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: DC
COUNTRY: US
ZIP: 2003
ZIP: 2004
COMPUTER READABLE FORM:
MEDIUM TYPE: 3+ Flo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-442-629-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIENYKKQARNGLGKDHEILRRRIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGAKELWFFLQSELKKLKHLEGNELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGDWR 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                 STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: US
                                                                                                                                                      APPLICANT: TANIGUCHI, Naoyuki
APPLICANT: TANIGUCHI, Naofumi
APPLICANT: SHIBA, Tet
APPLICANT: SHIBA, Tet
APPLICANT: YANAGIDANI, Shusaku
TITLE OF INVENTION: Alpha 1-6 Fucosyltransferase
NUMBER OF SEQUENCES: 15
ADDRESSEE: Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3+ Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WordPerfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,805A
FILING DATE: 7 JAN 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 23 JAN 1997
PELLING DATE: 23 JAN 1997
APPLICATION NUMBER: PCT/JP97/00171
APPLICATION NUMBER: JP 162813
APPLICATION NUMBER: JP 161648
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JAN 1996
APPLICATION NUMBER: JP 10365
ATTORNEY/AGENT INFORMATION:
NAME: TOFFENETI, JUNITH L.
REGISTRATION NUMBER: 39,0486
PREGISTRATION NUMBER: 39,0486
                                                                                         Sequence 2, Application US/08913805A
Patent No. 6054304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 antino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 93.6'
Matches 538; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-913-805A-2
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WordPerfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,805A
PILING DATE: 7 JAN 1998
CLASSIFICATION: 435
PRICH APPLICATION: A35
PRICH APPLICATION DATA:
APPLICATION NUMBER: PCT/JP97/00171
                                                                                                                                                                                          FILING DATE: 23 JAN 1997
APPLICATION NUMBER: PCT/UP97/00171
FILING DATE: 23 JAN 1997
APPLICATION NUMBER: DF 12260
FILING DATE: 23 JUL 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 101648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JAN 1996
ATTOWNEY/AGENT IRPORMATION:
NAME: TOFFENET, JUNIBBE: JP 048
REFERENCE/DOCKET NUMBER: 2356/3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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Best Local Similarity
Matches 25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                       61 RRMAESLRIPEGPIDOGPASGRVRALEGOFWKAKEQIENYKKOTKNGPGKDHEILRRRIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 LILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVNDKNIQVVELPIVDSLHPR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 LALESHNWRYATGGWETVFRPVSETCTDRSGSSTGHWSGEVKDKNVQVVELPIVDSVHPR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 PPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVI 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 GVHVRRTDKVGTEAAFHPIEEYMVHVEEHFQLLARRMQVDKKRVYLATDDPTLLKEAKTK 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 YSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIMQ 480
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                                                                                                                                                                                                                                                                                                                     NGAKELWFFLQSELKKLKHLEGNELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGDWR
                                                                                                                                                                                                                                                                                            1 MRAWIGSWRWIMLILFAWGTLLFYIGGHLVRDNDHPDHSSRELSKILAKLERLKQQNEDL
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                                                                                                                                                                                                        Length 575;
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STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20036
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GENERAL INFORMATION:
APPLICANT: TANIGUCHI, Naoyuki
APPLICANT: UOZUMI, Naofumi
APPLICANT: SHIBA, Tetsuo
APPLICANT: SANAGIDANI, Shusaku
TITLE OF INVENTION: Alpha 1-6 Fucosyltransferase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                   Query Match 94.3%; Score 2910; DB 3; Best Local Similarity 93.6%; Pred. No. 2.6e-265; Matches 538; Conservative 14; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGINRKLGKTGLYPSYKVREKIETVKYPTYPEAEK 575
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                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/08913805A
Patent No. 6054304
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                            US-09-442-629-2
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Gaps
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Patent No. 6291219

GENERAL INFORMATION:

APPLICANT: TANIGUCHI, Nacyuki

UOZUMI, Nactumi.

SHIBA, Tetsuo

YANGAIDANI, Shusaku

TITLE OF INVENTION: Alpha 1-6 Fucosyltransferase

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Remyon & Kenyon

STREET: 1025 Connecticut Avenue, N.W., Suite 600

CITY: Mashington
                                                                                                                                                                                                             Indels
                                                                                                                                                          4.2%; Score 131; DB 3; ilarity 100.0%; Pred. No. 1e-05; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: DC
COUNTRY: US
ZIP: 20036
ZONDUTER READABLE FORM:
MEDIUM TYPE: 3+ Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WordPerfect 6.1 Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/442,629
PRILIG DATE: 18-No. 6291219-1999
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/913,805A
FILING DATE: 7 JAN 1998
APPLICATION NUMBER: PCT/JP97/00171
                                                                                                                                                                                                                                                          352 KLGFKHPVIGVHVRRTDKVGTEAAF 376
                                                                                                                                                                                                                                                                                       1 KLGFKHPVIGVHVRRTDKVGTEAAF 25
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                        , MOLECULE TYPE: peptide US-08-913-805A-12
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509 AVYPHKPRIEEE (PMEPGDIIGVAG----NHWDGYSKGINRKLGKIGLYPSYKVREKIET 564
                                                                             509 AVYPHKPRTEEEIPMEPGDIIGVAG----NHWDGYSKGINRKLGKTGLYPSYKVREKIET
                      Gaps
                    10;
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                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OSTEON INC.
TITLE CANT: OSTEON INC.
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09127
  38.0%; Pred. No. 0.012; tive 12; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.012;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 221, Application US/08630915A Patent No. 6309820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPARKS, Andrew B.
HOFFMAN, No. 6309820h
KAY, Brian K.
FOWLKES, Pana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McCONNELL, Stephen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Paul C. Steinhardt
REGISTRATION NUMBER: 30,806
REFERENCE/DOCKET NUMBER: FP-N
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORN:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.0%;
Best Local Similarity 38.0% Matches 27; Conservative
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Best Local Similarity 38.0%
Matches 27; Conservative
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                                                                                                                                       565 VKYPTYPEAEK 575
                                                                                                                                                             : | : |::
73 IDNPLHEAAKR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 IDNPLHEAAKR E3
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APPLICANT: SPARKS
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USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-630-915A-221
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OSTEOSA INC.
TITLE OF INVENTION: Osteoclast Growth Regulatory Factor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
4.2%; Score 131; DB 3; Length 25
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08950
                                                                           FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JAN 1996
ATTORNEY/AGENT INFORMATION:
NAME: TOFFERENT, JUDITH L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 2356/3
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.7%; Score 114;
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                      APPLICATION NUMBER: JP 192260
FILING DATE: 22 JUL 1996
APPLICATION NUMBER: JP 162813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352 KLGFKHPVIGVHVRRTDKVGTEAAF 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KLGFKHPVIGVHVRRTDKVGTEAAF 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application PC/TUS9608950 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          TELEPHONE: 202-429-1776
TELEFAX: 202-429-0796
                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Paul C. Steinhardt
REGISTRATION NUMBER: 30,806
REFERENCE/DOCKET NUMBER: FP-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: SEGUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US96-08950-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: I
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45 KILAKLERLKQQNEDLRRMAESLRIPEGPIDQGTATGRV-RVLEEQLVKAKEQIENYKKQ 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 MEESNKARAAHSFVVTEFE--TTVCSLEELLRTEQQRLEKNEDQLKILTMELOKK---- 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          449 ENKQ------FEKIAEELKGTEQELIGLLQAREKEVHDLEIQLTAITTSEQYYSKE 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ARNGLGK---DHEILRRRIENGAKELWFFLQSELKKLKHLEG-----NE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 EAKDLTELVORRI-TYLONPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 ILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVNDKNIQVVELPIVDSLHPRP 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 PYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 VHVRRTDKVGTEAAFHPIEEYMVHVEEHF--QLLARRMQVDKKRVYL---ATDDPTLLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 113.5; DB 3; Length 976;
Pred. No. 0.14;
67; Mismatches 171; Indels 139; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 AK-----TKYSNYEFISD-NSISWSAGLHNRYTENSLRGVILDI 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     499 VKDLKTELENEKLKNTELTSHCNKLS----LENKELTQETSDMTLEL 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :|: :|| : | :|
323 ELEDIKVSLQRSVSTQKALEEDLQIATKTICQLTE-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 LORHADEILLDLGHHERSIMTDLYYL--SOTDGAGDWRE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: TANIGUCHI, Naoyuki
APPLICANT: UOZUMI, Naofumi
APPLICANT: STHEA, TEEGRO
APPLICANT: YANAGIDANI, Shusaku
TITLE OF INVENTION: Alpha 1-6 Fucosyltransferase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenvor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/992,702
FILING DATE: 15-July-1997
ATTORNEY/AGENT INFORMATION:
NAME: HANSON, NO. 62324660man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5491
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08913805A Patent No. 6054304 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 3.18-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.7%;
Best Local Similarity 19.3%;
Matches 90; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 976 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-104-324B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   416
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And Methods For Identifying Pathogenic Markers In A Sample Of
No. 6232460mal Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    509 AVYPHKPRTEEEIPMEPGDIIGVAG----NHWDGYSKGINRKLGKTGLYPSYKVREKIET 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 ALYTFEPRIPDELYFEEGDIIYIIDMSDINWWKGTSK-----GRIGLIPSNYVAEQAES 87
POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.7%; Score 114; DB 4; Length 229;
38.0%; Pred. No. 0.013;
iive 12; Mismatches 22; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ozlem; Sahin, Ugur; Pfreundschuh, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: 1BM
                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFFTATION - TO A TREE T
                                                                                                                                                                         E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEE: Fulbright & Jaworski LLP
?: 666 Fifth Avenue
New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/104,324B
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Patent No. 6232460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 221:
SEQUENCE CHARACTERISTICS:
LENGTH: 229 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.7s
Best Local Similarity 38.08
Matches 27; Conservative
   TITLE OF INVENTION: POLY
TITLE OF INVENTION: DOMA
TITLE OF INVENTION: USIN
NUMBER OF SEQUENCE: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Ed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      565 VKYPTYPEAEK 575
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MOLECULE TYPE: peptide
US-08-630-915A-221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | : | :
88 IDNPLHEAAKR 98
                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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APPLICANT: T reci, O;
TITLE OF INVENTION: P
TITLE OF INVENTION: P
TITLE OF INVENTION: P
                                                                                                                                                                                                                                                                                New York
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CLASSIFICATION:
                                                                                                                                                                                                                                            CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY:
STATE: Ne.
10103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-104-324B-4
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APPLICANT: YEN, TIMOYCHY J.

APPLICANT: RATTHER, JEROME B.
TITLE OF INVENTION: NUCLEIC ACID ENCODING A
TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: DANN, DORFWAN, HERRELL AND SKILLMAN
STREET: 1601 MARKEY STREET, SUITE 720
CITY: PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DÀTA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.7%; Score 113; DB 3;
88.0%; Pred. No. 0.00054;
tive 1; Mismatches 2
PCT/JP97/00171
                                                                                                                                                                                                                                                            NAME: TOFFENDELL, JUGITH L.
REGISTRATION INDBER: 39,048
REFERENCE/DOUKET NUMBER: 2356/3
TELECOMMUNICATION INPORMATION:
TELEFFAN. 202-429-0796
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                         APPLICATION NUMBER: JP 162813
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JAN 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/353,700
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENI INFORMÁTION:
NAME: REED, JANET B.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION:
                      FILING DATE: 23 JAN 1997
APPLICATION NUMBER: JP 192260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 KOARNGLGKDHEKLRRRIENGAKEL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KOTKNGPGKDHEILRRRIENGAKEL 25
                                                                       FILING DATE: 22 JUL 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1, Application US/08353700
; Patent No. 5599919
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 26 amino acids
                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (215) 563-4100
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TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.74
Best Local Similarity 88.09
Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-442-629-3
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STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
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Patent No. 6291219

GENERAL INFORMATION:
APPLICANT: TANIGUCHI, Nacyuki
UOZUMI, Nacfumi
SHIBA, Tetsuo
YANAGIDANI, Shusaku
TITLE OF INVENTION: Alpha 1-6 Fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: 3+ Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WordPerfect 6.1 Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/913,805A
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APPLICATION NUMBER: US/09/442,629
FILING DATE: 18-NO. 6291219-1999
PRIOR APPLICATION DATA:
                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOCTWARE: Worderfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,805A
FILING DATE: 7 JAN 1998
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/D997/00171
FILING DATE: 23 JAN 1997
APPLICATION NUMBER: JP 192260
FILING DATE: 22 JUL 1996
APPLICATION NUMBER: JP 162813
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JAN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JAN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JAN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JAN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JAN 1996
ATTORNEY AGENT THRORMATION:
                 MEDIUM TYPE: 3+ Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Toffenetti, Judith L. REGISTRATION NUMBER: 39,048 REFERENCE/DOCKET NUMBER: 23 TELECOMMUNICATION INFORMATION: 202-429-1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
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COMPUTER READABLE FORM:
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Best Local Similarity 88.04
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
COMPUTER READABLE FORM: MEDIUM TYPE: 3+ Flop
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US-09-442-629-3
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FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                      445 VK-QQLENNLEEFKQKLCRAEQAFQ------ASQIKENELRRSMEEMKKENNLLK 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 NPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQNW----RYATGGW 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETVFRPVSETCTDRSGLSTGHWSGEVNDKNIQVVELPIV------DSLHPRPPYLP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----WWVSQFVKYLIRPQPWL 342
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APPLICANT: Rattner, Jerome B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use
                                                                                                                                                                                                                                                                                           140 LEGNELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGDWREKEAKDLTELVQRRITYLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399 - VDKKRVYLATDDPTLLK-EAKTKYSNYEFISDNSISWSAGLHNRYTEN----SLRGV
                                                                                                                                                                                                                                                                      29 LVRDNDHPDHSSRELSKILAKLERLKQQNEDL---RRMAESLRIPEGPIDQGTATGRVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----BQLNDKLSKTEKESKALLSALBLKKKEYEELKEEKTLFSCWKSENEKLLTQ----M
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                    tch 3248; Score 113; DB 1; Length 3248; al Similarity 19.3%; Pred. No. 1; 102; Conservative 86; Mismatches 176; Indels 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 ILDIHFLSQADFLVCTFSSQVCRVAYEIM-QTLHPDASANFHSLDDI 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---LSNEIMDKDRCYODLHAEYESLRDL 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 LAVPEDLADRLLRVHGDPAV-----
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APPLICATION NUMBER: PCT/US9S/16216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application PC/TUS9516216 GENERAL INFORMATION:
                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, DOX
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732 VEDLEHKLOL---
                                                                                                                        ORGANISM: HUMAN
                                                                                 ANTI-SENSE: NO ORIGINAL SOURCE
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Sequence 63, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffals, R.
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve;
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 LEGNELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGDWREKEAKDLTELVQRRITYLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 LVRDNDHPDHSSRELSKILAKLERLKQQNEDL---RRMAESLRIPEGPIDQGTATGRVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.7%; Score 113; DB 5; Length 3248; Best Local Similarity 19.3%; Pred. No. 1; Matches 102; Conservative 86; Mismatches 176; Indels 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 ILDIHFLSQADFLVCTFSSQVCRVAYEIM--QTLHPDASANFHSLDDI 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 LVRTTAQYDQAS---TKYTALEQKLKKLTEDLSCQRQNAESARCS--
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                                                 US 08/353,700
                                                                                                                        NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                 SS: not relevant not relevant
                                                                      FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
                                                                   09-DEC-1995
                                                                                                                                                                                                 TELEPHONE: (215) 563-41(
TELEFAX: '(215) 563-4044
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: not recommodification MOLECULE TYPE: protein
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                  ENYKKQARNGIG--KDHEILRRRIENGAKE-----LWFFLQSELKKL-----KHL 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EG--NELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGDWREKEAKDLTELVQRRITYL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 QNPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLLLESQNWRYA---- 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 KVTRD---IRKIAMAFNKN-AYGAAKN----AFDKAFGSLETCLYKSLTKSYRDTFCDYK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TGGWETVFRPVSETCTDRSGLSTGHWSGEVNDKNIQVVELPIVDSLHPR- 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 RAKILPDENNSARAEQRFREVKDHWEDLN--ETVFWVKE--DGRIDIEVLTAVGGWPDRY 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 PPYLPLAVPED-----LADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATK--- 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :| | :| | :| | | : | | 355 PEHLILEKRKDKVMSHQLWEATMRVKEAEVTYSVAR-VAFEKDGSQQNQKKFQEKTKERL 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 ------KLGFKHPVIGVHVRRTD---KVGTEAAFHPIEE----- 381
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                                                                                                                                                                                                                       Query Watch 3.6%; Score 110.5; DB 4; Length 644; Best Local Similarity 21.0%; Pred. No. 0.14; Matches 103; Conservative 72; Mismatches 191; Indels 125;
CURRENT APPLICATION NUMBER: US/09/198,452A CURRENT FILING DATE: 1998-11-24 NUMBER OF SEQ 1D NOS: 6849 SEQ 1D NO 63 LENGTH: 644
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Job time : 16.5 secs
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; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-63
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1 MRAWIGSWRWIMLILFAWGT.....YKVREKIETVKYPTYPEAEK 575
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
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Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
	3085	100.0	575	1	US-09-971-773-24	Sequence 24, Appl
7	3024	98.0	575	11	US-09-971-773-23	Sequence 23, Appl
e.	2992	97.0	575	σ	US-09-839-136-10	Sequence 10, Appl
4	2903	94.1	575	σ	US-09-839-136-2	Sequence 2, Appli
S	2658	86.2	515	15	US-10-106-698-4658	Sequence 4658, Ap
9	432	14.0	82	σ	US-09-864-761-34720	Sequence 34720, A
٠ ٦	426	13.8	81	σ	US-09-864-761-46107	Sequence 46107, A
80	127	4.1	1055	12	US-10-369-493-12504	Sequence 12504, A
0	123	4.0	485	12	US-10-104-047-3419	Sequence 3419, Ap
10	122	4.0	25	σ	US-09-839-136-12	Sequence 12, Appl
11	118.5	3.8		12	US-10-117-937-596	Sequence 596, App
12	116.5	3.8		12	US-10-369-493-22825	Sequence 22825, A
13	116.5	3.8		12	US-10-369-493-6527	Sequence 6527, Ap
14	116	3.8	678		US-10-369-493-5427	Sequence 5427, Ap
15	116	3.8		15		Sequence 273, App

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317, 6931, 73, 73, 73, 73, 73, 73, 74, 74, 74, 74, 74, 74, 74, 74, 74, 74	Sequence 66, Appl Sequence 64, Appl Sequence 2556, Ap Sequence 1056, Ap Sequence 1056, Ap Sequence 10297, A
US-10-177-293-317 US-10-369-493-6931 US-09-893-519A-73 US-09-879-957-221 US-10-369-493-5128 US-10-369-493-5128 US-10-369-493-5129 US-10-094-749-3191 US-10-028-246A-105 US-10-017-216-6 US-10-017-216-4 US-10-017-216-4 US-10-017-216-4 US-10-017-216-4 US-10-017-218-4 US-10-017-218-4 US-10-017-218-4 US-10-032-189-79 US-10-389-493-1330 US-10-389-493-1330 US-10-389-496-64	US-10-262-445-66 US-10-262-445-64 US-10-369-493-21643 US-10-369-493-21643 US-10-289-762-1056 US-10-369-493-10297 US-10-132-350-42
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## ALIGNMENTS

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1 MRAWTGSWRWIMLILFAWGTLLFYIGGHLVRDNDHPDHSSRELSKILAKLERLKQQNEDL
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Best Local Similarity 100.0%; Pred. No. 2.3e-271;
Matches 575; Conservative 0; Mismatches 0; Indels 0;
                                                                                                     APPLICANT: Micros SATOH
APPLICANT: Kazuyasu NAKAMURA
APPLICANT: Kazuyasu NAKAMURA
APPLICANT: Razuyasu NAKAMURA
APPLICANT: Toyohida SHINKAMA
APPLICANT: Norbox YAMASKI
APPLICANT: Notox YAMASKI
APPLICANT: No. US20030115614Aluo HANAI
TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING
FILE REFERENCE: 249-202
CURRENT PELLATION NUMBER: US/09/971,773
CURRENT PELLOATION NUMBER: US/09/971,773
CURRENT PELLOATION NUMBER: US 60/268,926
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 73
SOFWARE: Patentin Ver: 2.1
SSQ ID NO 24
Sequence 24, Application US/09971773
Publication No. US20030115614A1
GENERAL INFORMATION:
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180 180 240 240 480 480 540 540

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241 LILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVKDKNVQVVELPIVDSLHPR 300
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RRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIENYKKQARNGLGKDHEILRRRIE
                          61 RRWAESLRIPEGPIDQCTATGRVRVLEEQLVKAKEQIENYKKQARNDLGKDHEILRRRIE
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                                                                                                                121 NGAKELWFFLQSELKKLKHLEGNELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGDWR
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Sequence 10, Application US/09839136
Fatent No. US20020081694A1
GENERAL INFORMATION:
TITLE OF INVENTION: ALPHA 1-6 FUCOSYLTRANSFERASE
FILE REFERENCE: 2356-7
CURRENT APPLICATION NUMBER: US/09/839,136
CURRENT FILING DATE: 2001-04-23
FRIOR PLILING DATE: 1999-11-18
FRIOR FILING DATE: 1999-11-18
FRIOR FILING DATE: 1999-11-18
FRIOR APPLICATION NUMBER: 05/442,629
FRIOR FILING DATE: 1999-11-18
FRIOR FILING DATE: 1999-11-18
SPRIOR FILING DATE: 1999-11-18
SPRIOR FILING DATE: 1999-11-07
FRIOR FILING DATE: 1999-11-07
FRIOR FILING DATE: 1997-01-07
SPRIOR FILING DATE: 1997-01-07
FRIOR FILING DATE: 1997-01-07
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Best Local Similarity 96.2%
Matches 553; Conservative
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CRGANISM: Homo sapiens
US-09-839-136-10
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                                                                                                                      121 NGAKELWFFLOSELKKLKHLEGNELORHADEILLDLGHHERSIMTDLYYLSGTDGAGDWR
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                             RRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIENYKKQARNGLGKDHEILRRRIE
                                                                                     NCAKELWFFLQSELKKLKHLEGNELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGDWR
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APPLICANT: Micson SATOH
APPLICANT: Kazuyasu NAKAMURA
APPLICANT: Kazuyasu NAKAMURA
APPLICANT: Kazuyasu NAKAMURA
APPLICANT: Toyohida SHINKAWA
APPLICANT: Naoko YAMANE
APPLICANT: Naoko YAMANE
APPLICANT: No. USZ030115614Aluo HANAI
APPLICANT: No. USZ030115614Aluo HANAI
APPLICANT: No. USZ030115614Aluo HANAI
APPLICANT: No. USZ030115614Aluo HANAI
APPLICANT: NO. USZ0301015614Aluo HANAI
APPLICANTO NUMBER: US/09/971,773
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/268,926
PRIOR APPLICATION NUMBER: US 60/268,926
PRIOR APPLICATION NUMBER: US 60/268,926
RROR APPLICATIO
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Pred. No. 8.1e-266;
9; Mismatches 5;
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Publication No. US20030115614A1
GENERAL INFORMATION:
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97.6%;
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; ORGANISM: Cricetulus griseus
US-09-971-773-23
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Best Local Similarity 97.6
Matches 561; Conservative
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APPLICANT: Mitsuo SATOF
APPLICANT: Kazuyasu NAF
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Sequence 4659, Application US/10106698

Sequence 4659, Application No. US2030109590A1

GENERAL INFORMATION:
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides;
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT APPLICATION NUMBER: DCT/US00/26524

PRIOR PILING DATE: 2002-03-27

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-01-03

PRIOR PILING DATE: 1999-11-03

PRIOR PILING DATE: 1999-11-03

NUMBER: PA FEATH IN VOICE: 8564

SOFTWARE: PA FEATH IN VET: 3.0

SEQ ID NO 4658

LENGTH: 515
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                                                                   LILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVNDKNIQVVELPIVDSLHPR
                                                                                                                                      PPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEBATKKLGFKHPVI
                                                                                                                                                                                                         GVHVRRIDKVGTSAAFHPIEEYMVHVEEHFQLLARRMQVDKKRVYLAIDDPTLLKEAKTK
EKEAKDLTELVQRRITYLQNPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRT
                    191 EKEAKDLTELVQXRITYLQNPKDCSKAKKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRT
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96.1%; Pred. No. 1.3e-232;
tive 12; Mismatches 8;
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Best Local Similarity
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US-10-106-698-4658
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                                                                                       PPYLPLAVPEDLADRLVRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVI
                                                                      EKEAKDLTELVORRITYLONPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTORT
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APPLICANT: Nacyuki TANIGUCHI et al.
APPLICANT: Nacyuki TANIGUCHI et al.
TITLE OF INVENTION: ALPHA 1-6 FUCOSYLTRANSFERASE;
FILE REPERENCE: 2336-7
CURRENT APPLICATION NUMBER: US/09/839,136
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/442,629
PRIOR FILING DATE: 1999-11-18
PRIOR APPLICATION NUMBER: 08/913,805
PRIOR APPLICATION NUMBER: PS/10171
PRIOR APPLICATION NUMBER: PS/10171
PRIOR APPLICATION NUMBER: PCT/JP97/00171
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
SROID NO SEQ ID NOS: 15
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 94.1%; Score 2903; DB 9; Best Local Similarity 93.4%; Pred. No. 8.1e-255; Matches 537; Conservative 14; Mismatches 24;
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; Patent No. US20020081694A1
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ORGANISM: Pig
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US-09-839-136-2
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US-09-839-136-2
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Sequence 46107, Application US/09864761

Sequence 46107, Application US/09864761

Sequence 46107, Application US/09864761

SERVERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David R.

TITLE OF INVENTION: HUWAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUWAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL CURRENT TILING DATE: 2000-05-23

FRIOR APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2000-05-24

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-06-33

PRIOR PLICATION NUMBER: US 60/236,36

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/0066

PRIOR PLING DATE: 2001-01-30

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HER INFORMATION: EXPRESSED IN PIACENTA, SIGNAL = 4.6
HER INFORMATION: EXPRESSED IN PIBLIO0, SIGNAL = 3.6
HER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.5
HER INFORMATION: EXPRESSED IN LONG, SIGNAL = 5.1
HER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3
HER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.7
HER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3
HER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.9
HER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.9
HER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.9
HER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.9
HER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.9
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HER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.9
HER INFORMATION: EXT. HUMAN HIT: AW002060.1, EVALUE 7.00e-44
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96.3%; Pred. No. 1.7e-31;
tive 2; Mismatches 1;
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PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00662
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APPLICATION NUMBER: PCT/US01/00663
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                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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FERTURE:
OTHER INFORMATION: M
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OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER 
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SEQ ID NO 34720
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SEQUENCE 34720, APPLICATION STATE OF APPLICATION STATE OF APPLICANTINE RAINE, DAVIG R.

APPLICANT: RAINE, DAVIG R.

APPLICANT: RAINE, DAVIG R.

APPLICANT: HARNEL J. DAVIG R.

APPLICANT: HARNEL J. DAVIG R.

APPLICANT: HARNEL J. DAVIG R.

APPLICANT: Chen, WENTERSHOWN HOWERSER SERVERSION ANALYSIS BY MICROARRAY CURRENT FILING DATE: 2001-05-23

PRIOR PLITA OF INVERTION WINDERS: US/05/064,761

CURRENT FILING DATE: 2001-05-24

PRIOR PLITA OF DAVIE STATE OF STATE OF STATE OF STATE OF STATE OF STATE APPLICATION NUMBER: US/05/064,761

PRIOR APPLICATION NUMBER: US/05/06-03

PRIOR PLITA OF STATE OF STA
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305 PLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVIGVHV 364
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                                                  245 PLAVPEDLADRLVRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVIGVHV
                                                                                                                                                                                          365 RRTDKVGTEAAFHPIEEYMVHVEEHFQLLARRMQVDKKRVYLATDDPTLLKEAKTKYSNY
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US-09-864-761-34720
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                                          829 SQ-KGGIEEEIQNLQNKIMEVGGVRLRSQKAKVDGLKEQISLLSEEISNAEVARSKNEKL 887
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                                                                                            140 LEGNELOR-HADBILLDLGHHERSIMTDLYYLSQTDGAGDWREK--EAKDLT 188
                                                                                                                    Sequence 3419, Application US/10104047

Sequence 3419, Application US/10104047

Publication No. US20030236392A1

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA

FILE REFERENCE: HI-A0105

CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT FILING DATE: 2002-03-25

PRIOR PILING DATE:

NUMBER OF SEQ ID NOS: 4096

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 485;
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TITLE OF INVENTION: ALFHA 1-6 FUCOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 12, Application US/09839136; Patent No. US20020081694A1; GENERAL INFORMATION:
  102 KQARNGLGKDHEXLRRRI-
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US-10-104-047-3419
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Best Local Similarity
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APPLICANT: Gao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Gater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Marker S.
APPLICANT: Goldman, Marker MITH IMPROVED PROPERTIES
FILLE REPERENCE: 38-10 (5205.)
FILLE REPERENCE: 38-10 (5205.)
CURRENT APPLICATION NUMBER: US (0/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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25.6%; Pred. No. 0.041;
tive 38; Mismatches 60; Indels 30
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED BARIN, SIGNAL = 1.3
OTHER INFORMATION: SMISSPROT HIT: Q9VLZ7, EVALUE 6.40e+00
OTHER INFORMATION: EST_HUMAN HIT: AMO02060.1, EVALUE 5.00e-43
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                 PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER: OF SEQ ID NOS: 49117
SOFTWARE: Annowax Sequence Listing Engine vers. 1.1
SEQ ID NO 46107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 426; DB 9;
Pred. No. 5.8e-31;
2; Mismatches 1;
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OTHER INFORMATION: unsure at all Xaa locations
  APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12504, Application US/10369493
Publication No. US20030233675A1
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ORGANISM: Homo sapiens
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es 78; Conserv
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPERSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(5.26.2) B
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22825
LENGTH: 919
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                                                                                                                                                                    302 PYLPLAVPEDLADRILLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVIG
                                                                                                                                                                                               449 ENKO------FEKIAEELKGTEGELIGLLQAREKEVHDLEIQLTAITTSEQYYSKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 VFRPVSETCTDRSGLSTGHWSGEVNDKNIQVVELPIVDSLHPRPPYLPLA----VPEDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     632 GITAYRSLDDLLEKAREALEGVDKELSAIERRLEEARRLKEEAAKLKWEAEQVMKRLEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 ONPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLI-LESQNWRYATGGWET
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                                                                                                                                                                                                                                                                  362 VHVRRIDKVGTEAAFHPIEEYMVHVEEHF--QLLARRMQVDKKRVYL---ATDDPTLLKE
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                                                                                                        363 MEESNKARAAHSFVVTEFE--TTVCSLEELLERTEQQRLEKNEDQLKILTMELQKK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12; Length 919;
                                                                                                                                                                                                                                                                                                                                                                                               499 VKDLKTELENEKLKNTELTSHCNKLS----LENKELTQETSDMTLEL 541
                                                                                                                                                                                                                                                                                                                                                               417 AK------TKYSNYEFISD-NSISWSAGLHNRYTENSLRGVILDI 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.8%; Score 116.5; DB 12; 22.5%; Pred. No. 0.3; tive 70; Mismatches 160;
| :|: || :| : : | ELEDIKVSLQRSVSTQKALEEDLQIATKTICQLTE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 22825, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
3.8%
Best Local Similarity 22.5%
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Aeropyrum pernix US-10-369-493-22825
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US-10-369-493-22825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 REETROVYMDLINNIEKMITAHGELRVQAENSRLEMHFKLKEDYEKIQHLEQEYKKEIND 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 122; DB 9; Length 25; pred. No. 0.00043; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 LQRHADEILLDLGHHERSIMTDLYYL--SQTDGAGDWRE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12;
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Best Local Similarity 19.5%; Pred. No. 0.22;
Matches 91; Conservative 66; Mismatches 1
                      CURRENT APPLICATION NUMBER: US/09/839,136
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/442,629
PRIOR FILING DATE: 1999-11-18
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1997-01-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
SEQ ID NOS: 25
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/117,937
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR FILING DATE: 2001-04-06
PRIOR PILING DATE: 2001-10-07
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2001-11-07
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 602
SOFTWARE: PASISEQ for Windows Version 4.0
SSOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 596
LENGTH: 976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 596, Application US/10117937
Publication No. US20030220239A1
GENERAL INFORMATION:
APPLICANT: CTL IMMUNO THERAPIES CORP.
APPLICANT: SIMMIN, Jul.
APPLICANT: SIMMIN, Jul.
APPLICANT: LIU, Liping
APPLICANT: LIU, Liping
APPLICANT: XE. Zhidong
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: CTLIMM.027A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLGFKHPVIGVHVRRTDKVGTCAAF 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.0%;
Best Local Similarity 96.0%;
Matches 24; Conservative (
                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Primer
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US-10-117-937-596
       FILE REFERENCE: 2356-7
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US-10-117-937-596
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Sequence 5427, Application US/10369493

Publication No. US20030233675A1

Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei

APPLICANT: Gland: Barry Greeory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXFRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXFRESSION OF MICROBIAL PROTEINS IN PLANTS WITH IMPROVED PROPERTIES
FILE REPRENCE: 38-10 (52052)
FILE REPRENCE: 38-10 (52052)
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
NUMBER OF SEQ ID NOS: 47374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 YEIEIRSNPLKUKAIQLQETLDTLKKQEEKLMEDMQSALTPEA---WRDKMSENMKQLNA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #12 DLVVIEKQHKTVKDQISLASEELHEYDSQGEAQIMAHHTKYLDLLSKSTMLDDTTENYPQ 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 TLILESQNWRYATGGWETVFRPVSE------TCTDRSGLSTGHWSGEVNDK---- 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----NIQVVELPI---VDSLHPRPPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVK 333
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472 QIVIYQQDIEEFSDAVVLILRKISANLKKVNLEDQITDLDERGLTL--QTGNVDELKEMH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 HSSRELSKILAFLERLKOONEDLRRMAESLRIPEGPIDOGTATGRVRVLEEQLVKAKEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENYKKQARNGLGKDHEILRRRIENGAKELWFFLQSELKKLK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 116; DB 12; ; Pred. No. 0.21; 81; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 273, Application US/10205823; Publication No. US20030:08963A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gammavarapu, Manjula
APPLICANT: Gorbatchevé, Bella
APPLICANT: Hoersch, Schastian
APPLICANT: Kamatkar, Shubhangi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.8%;
18.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.8%
Query Match
Best Local Similarity 18.1%
Matches 86; Conservative
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                                                                                                                                                                                                                                                                                                                      Sequence 6527, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Gidman, Barry S.
APPLICANT: Glodman, Barry S.
APPLICANT: Glodman, Barry S.
APPLICANT: Grown C.
CURRENT APPLICATION NUMBER: US/10/369, 493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 CSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQNWRYATGGWETVFRPVS 263
808 REIEVKAIGGNGAYRPLE--AVSGGERTVLALSFVLALNKAVGGKLGFLALDEPTANLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTKYSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADF--LVC--TFSSQVCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SLRIPEGPIDQGTATGRVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGDWREKEAKDLTELVQRRITYLQNPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETCTDRSGLSTGHWSGEVNDKNIQVVELP-IVDSLHPRPPYLPLAVPEDL-ADRLLRVHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTDKVGTEAAFHPIE----EYMVHVEEHFQLLAR------RMQVDKKRVYLATDDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12; Length 1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-----LLKEAKTKYSNYEFISD---NSISWSAGLHNRY-TENS 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.8%; Score 116.5; DB 12;
19.1%; Pred. No. 0.97;
tive 69; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1095 LKVAQENIDEITK-----QKHDV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 ELSKILAKLERLKOONEDLRRMAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 19.1
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 6527
                                                                                                                                                                 474 V 474
                                                                                                                                                                                                           915 V 915
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APPLICANT: Anderson, Dustin
TITLE OF INVENTION: MCFLORES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: MCFLORES
TITLE OF INVENTION: MFFHODS FOR IDENTIFFCATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: HFRAPY OF PROSTATE CANCER
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
CURRENT PELLING DATE: 2002-07-25
FRICH FILING DATE: 2001-07-25
FRICH FILING DATE: 2001-08-22
FRICH FILING DATE: 2001-08-22
FRICH RELICATION NUMBER: 60/325,020
FRICH APPLICATION NUMBER: 60/325,020
FRICH APPLICATION NUMBER: 60/325,020
FRICH APPLICATION NUMBER: 60/341,746
FRICH FILING DATE: 2001-12-12
FRICH FILING DATE: 2001-12-12
FRICH FILING DATE: 2001-03-05
FRICH FILING DATE: 2002-03-05
FRICH FACESTORES FACES FACESTORES FACES                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  954 RRMKLEMBAKRKQEEBERKKREDDEKRIQAEVEAQLARQKEEBSQQQAVLEQERRDRELA 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LRDTINTSC 1093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 LDLGHHERSIMTDL----YYLSQTDGAGD--WREKEAKDLTELVORRITYLQNPKDCSKA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 RKLVCNINKGCGYGCQLHHVVYCPMIAYGTQRTLILESQNWRYATGGWETVFRPVSETCT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 D------RSGLSTGH-WSGEVNDKNIQ------VVELPIVDSLHPRPPYLPLA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 ------VPEDLADRLLRV-----HGDPAV----WWVSQFVKYLIRPQPWLEKEIE 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     905 SSEELLSALQKKKKQQEEAAERLRRIQEBME------KERKRREEDEKRRRKEEEE 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 NYKKQARNGLGKDHEILRRRIENGAKELWFFLQSELKKLKHLEGN-----ELQRHADEIL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 SSRELSKILAKLERLKQONEDLRRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIE 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.8%; Score 116; DB 15; Length 1285; Best Local Similarity 19.7%; Pred. No. 0.56; Matches 71; Conservative 51; Mismatches 130; Indels 108; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
US-10-205-823-273
Zhao, Xumei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----- 6901
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Search completed: February 2, 2004, 08:52:04 Job time : 218 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

February 2, 2004, 08:39:43; Search time 17 Seconds (without alignments) 3252.764 Million cell updates/sec Run on:

Title: Perfect score:

US-09-971-773-24 3085 1 MRAWIGSWRWIMLILFAWGT......XKVREKIETVKYPTYPEAEK

575

Scoring table: Sequence:

283308 seqs, 96168682 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		æ				
Result		Query				
No.	Score	Match	Length	8	QI	Description
1	3003	97.3	575	Н		glycoprotein 6-alp
7	982	31.8	818	~	T32154	prot
e	N	4.1	946	7	S28061	
4	125.5	4.1	845	N	148176	synaptonemal compl
2	125	4.1	1025	7	H86250	П
9	118	3.8	1173	N	T43527	- 1
7	118	3.8	1727	<b>N</b>	T50073	myosin-like coiled
œ	117	3.8	1744	7	F86161	F1003.10 protein -
σ	117	3.8	1871	~	D96796	probable heat shoc
10	117	٠	1955	7	T30934	myosin-like protei
11	116.5	٠	919	7	B72765	hypothetical prote
12	116.5	3.8	1992	Н	S02771	myosin heavy chain
13	_	•	678	0	H88187	protein C18H9.8 [i
14	115.5	3.7	1427	~	822695	restin - human
15	115	3.7	1137	N	T19414	hypothetical prote
16	. 115	•	1156	N	B70356	chromosome assembl
17	115	3.7	1325	N	S16129	dynein-associated
18	-4	•	755	~	T34567	hypothetical prote
19		3.7	101	~	T13055	dynamin associated
20	113.5		1023	7	T33338	hypothetical prote
21	113.5	3.7	2020	~	T21174	
22	113	3.7	1094	~	T13053	dynamin associated
23	112.5	3.6	832	N	H72278	alpha-mannosidase-
24	112.5	3.6	1270	~	T09194	adaptor protein in
25	٠	3.6	2007	Н	B43402	myosin heavy chain
56	111.5	•	1281	N	JC5368	dynactin 1 - mouse
27		3.6	1392	~	A43336	microtubule-vesicl
28	111.5	3.6	1935	Н	A37102	4
29	111	3.6	993	~	S49461	synaptonemal compl

citron - mouse	centrosome associa	hypothetical prote	hypothetical prote	conserved hypothet	protein F54C1.1 [i	carbamoy1-phosphat	hypothetical prote	probable chromosom	glycoprotein A - m	myosin beta heavy	gamma response I p	gamma response I p	myosin heavy chain	protein F55A8.2 [i	conserved hypothet
S68420	T08621	E86496	F81543	A70387	B87768	F89892	F72127	F71190	JE0120	806006	T48905	T49091	I48153	D88640	F75103
	N	a	~	7	0	0	7	~	7	н	a	~	~	N	2
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1597 2	2:142	542	542	978	581	1057	542	1179	1282	1935	589	1110	1934	521	380
3.6 1597 2	3.6 2442	3.6 542	3.6 542	3.6 978	3.6 581	3.6 1057	3.5 542	3.5 1179	3.5 1282	3.5 1935	3.5 589	3.5 1110	3.5 1934	3.5 521	3.5 380
111 3.6 1597 2	3.6	3.6	110.5 3.6 542	3.6	3.6	3.6	3.5	3.5	3.5	3.5	3.5	3.5	3.5	108.5 3.5 521	3.5

## ALIGNMENTS

RESULT 1	
glycoprotein 6-alpha N;Alternate names: a	glycoprotein 6-alpha-L-fucosyltransferase (EC 2.4.1.68) precursor - human N/Alternate names: alpha 1-6 FucT; GDP-L-fucose:N-acetyl-beta-D-glucosaminyl:6-alpha-L-f
C;Species: Homo sapiens (man) C;Date: 03-Dec-1999 #sequence	C.Species: Homo sapiens (man) C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Jun-2000 C.Accesion: 17542? Pr43:2
R; Yanagidani, S.; Uozumi, N.;	O'STUDY TOTALIN N.; Ihara, Y.; Miyoshi, E.; Yamaguchi, N.; Taniguchi, N.
A; Title: Purificatio A; Reference number:	A.Title: Durffication and cDNA cloning of GDP-L-Fuc:N-acetyl-beta-D-glucosaminide:alpha A:Reference number: JC5432; MUID:97279058; PMID:9133635
A; Accession: JC5432 A; Molecule type: mRNA	A
A; Residues: 1-575 < YAN1> A; Cross-references: DDBJ	A;Residues: 1-575 <yan1> A;Cross-references: DDBJ:)389289; NID:g2055306; PIDN:BAA19764.1; PID:g2055307</yan1>
A; Accession: PC4322	\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$
A; Residues: 68-87;35	AjMolecule Vye: plocell XResidues: 68-87352-376; C. Commant: This anothe rejelving the transfer of fuces from CDD-fuconvranceide to agna-
C, Genetics:	C.Commence. Mile emergine cacalyzes one transfer of faces from Of facepyrancers of ages.
A; Cross-references:	Ajdene: GDB:9786294; OMIM:602589
A; Map position: 14q23-14q23 C; Superfamily: human glycop	A;Map position: 14q23-14q23 C;Superfamily: human glycoprotein 6-alpha-L-fucosyltransferase
<pre>C;Keywords: glycosyl F;1-22/Domain: signa F;23-575/Product: gl</pre>	C;Keywords: glycosyltrans:erase; hexosyltransferase F;1-22/Domain: signal sequence #status predicted <sig> F;23-575/Product: glycoprótein 6-alpha-L-fucosyltransferase #status predicted <mat></mat></sig>
Operv Match .	97 3%: Score 3003: DB 1: Length 575:
Best Local Similarity Matches 555; Conserv	96.5%; Pred. No. 1.6e-194; arive 11; Mismatches 9; Indela
Qy 1 MRAWTG	1 MRAWTGSWRWIMLILFAWGTLLFYIGGHLVRDNDHPDHSSRELSKILAKLERLKQQNEDL 60
Db 1 MRPWTG	
Qy 61 RRMAES	RRMAESLRIPEGPIDGGTATGRVRVLEEGLVKAKEQIENYKKQARNGLGKDHEILRRRIE 120
DD 61 RRMAES	RRMAESLRIPEGPIQGPAIGRVRVLEEQLVKAKEQIENYKKQTRNGLGKDHEILRRRIE 120
Qy 121 NGAKEL	NGAKELWFFLQ;ELKKLKHLEGNELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGDWR 180
Db 121 NGAKEL	DEFL
Qy 181 EKEAKD	EKEAKDLTELVŲRRITYLQNPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRT 240
Db 181 EKEAKD	EKEAKDLTELVĮRITYLQNPKDCSKAKKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRT 240

LILESONWRYA;CGWETVFRPVSETCTDRSGLSTGHWSGEVNDKNIQVVELPIVDSLHPR 300

241 241

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Oy 406 LATDDPTLLKEAKTKYSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADFLVC 465	R;Meuwissen, R.L.J.; Offenberg, H.H.; Dietrich, A.J.J.; Riesewijk, A.; van Iersel, M.; FEMBO J. II. 5091-2100, 1992  EMBO J. II. 5091-2100, 1992  A;Title: A coiled-coil related protein specific for synapsed regions of meiotic prophase A; Reference number: S28061  A;Molecule type: mRNA A;Rosidues: 1-946 <mrda 1-946="" 1.9;="" 100="" 109;="" 162;="" 180;="" 20.6%;="" 24;="" 42="" 78;="" <mrda="" a;cross-references:="" a;rosidues:="" bast="" binding="" c;gantics:="" c;keywords:="" conservative="" dna="" elskilaklerelkqqnedlrrwaeslripegpidqctatgr-vrvleeqlvkakeqieny="" embl:x67805;="" gaps="" indels="" local="" match="" matches="" mismatches="" nid:957212;="" no.="" pid:957213="" pidn:caa48006.1;="" pred.="" query="" qy="" scp1="" similarity="" th=""  =""  <=""><th>151 EYERETRQVYUDLNNIEKMILAFEELRVQAENARLEMHFKLKEDHEKIQHLE-BEYÖK  148 HADEILLDLGHHERSIMTDLYLSQTDGAGDWREKEAKIQHLE-EEYÖK  150 EVNNKENQVSLLIJOSTEKENKÖMKDLTFLIEESRDKANQLEEKTKLQDENLKELNE  200 NPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESONWRYATGGWETVF  265 EKKDHLTSTKLQDENLKELNE  266 EKKDHLTS</th></mrda>	151 EYERETRQVYUDLNNIEKMILAFEELRVQAENARLEMHFKLKEDHEKIQHLE-BEYÖK  148 HADEILLDLGHHERSIMTDLYLSQTDGAGDWREKEAKIQHLE-EEYÖK  150 EVNNKENQVSLLIJOSTEKENKÖMKDLTFLIEESRDKANQLEEKTKLQDENLKELNE  200 NPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESONWRYATGGWETVF  265 EKKDHLTSTKLQDENLKELNE  266 EKKDHLTS
Qy         301         PPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVI 360           Db         301         PPYLPLAVPEDLADRLVWHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVI 360           Qy         361         GVHVRRTDKVGTEAAFHPIEEYWWHVEEHFQLLARRWQVDKKRVYLATDDFTLLKEAKTK 420           Db         361         GVHVRRTDKVGTEAAFHPIEEYWWHVEEHFQLLARRWQVDKKRVYLATDDFSLLKEAKTK 420           Qy         421         VSNYEFISDNSISWSAGLHNRYTENSLEGVILDIHFLSQADFLVCTFSSQVCRVAXEIMQ 480           Db         421         YPNYEFISDNSISWSAGLHNRYTENSLEGVILDIHFLSQADFLVCTFSSQVCRVAXEIMQ 480           Qy         481         TLHPDASANFHSLDDIYYFGGQNAHNQIAVYPHKPRTEEEIPWEPGDIIGVAGNHWDGYS 540           Qy         481         TLHPDASANFHSLDDIYYFGGQNAHNQIAVYPHYPRADEIPWEPGDIIGVAGNHWDGYS 540           Qy         541         KGINRKLGKTGLYPSYKVREKIETVKYPTYPBAEK 575           Db         541         KGINRKLGRTGLYPSYKVREKIETVKYPTYPBAEK 575	RESULT 2 T32154 hypothetical protein C10F3.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: T3154 R;Davidson, S:; Wohldmann, P. Submitted to the EMBL Data Library, September 1997 A;Accession: T32154 A;Reference number: Z21127 A;Accession: T32154 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Rotoss-references: EMBL;AF022968; PIDN:AAB69888.1; GSPDB:GN00023; CESP:C10F3.6 A;Kross-references: EMBL;AF022968; PIDN:AAB69888.1; GSPDB:GN00023; CESP:C10F3.6 A;Kross-references: EMBL;AF022968; PIDN:AAB69888.1; GSPDB:GN00023; CSP:C10F3.6 A;Kross-references: EMBL;AF022968; A;Appearimental source: strain Bristol N2; clone C10F3 C;Genetics: A;Gene: CESP:C10F3.6 A;App position: 57/2; 235/2; 258/3; 285/2; 315/3; 491/1; 544/3; 556/1; 64	982; 315/3; 45//3; 491/1; 544/3; 555/1; 926/1; 926/1; 982; DB 2; Length 818; No. 3.46-58; Smatches 191; Indels 50; Gaps 11; HUYDDDHPDHSRELSKILAKLERLKQONEDLRR 62:::::::::::::::::::::::::::::::::::

--IMTDLYYLSOTDGAG

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SGNW-WFAEVVV'PGGALVIDWVFADGPPKGAFLYDNNGYQDFHALVPQKLPEELYWLEEE 420
                                                                                                                                                                                                                                                                                                                                                     57 NEDLIRRMAESLE:IPEGPI-----DQGTATGRVRVLEEQLVKAKEQIENYKKQARNGLG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             537 LDAYMMDFVFSEKEDGGIFDNKNGLDYHLPVVGGISKEPPLHIVHIAVEMAPIAKVGGLG 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        753 KATTVSPTYAK:VAGNSVISAHLYKFHGIINGIDPDIWDPYNDNFI-----PVPYTSENV 807
                      A;Molecule type: DNA
A;Residues: 1-1025 <STO>
A;Cross-references: GB:AEC05172; NID:g4835785; PIDN:AAD30251.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 KDHEIL---RREIENGAKELWFFLQSELKKLKHLEG------NELQRHA-----
                                                                                                                                                                                                                                                       5 TGSWRWIMLILFAWGTLLF-YI-----GGHLVRDNDHPDHSSRELSKILAKLERLKQQ
                                                                                                                                                                                                                                                                                                                                                                                  -----INKGCGYGCQ------LHHVVYCFMIAYGTQRTLILESQNWRYATGGW
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                                                                                                                                                        4.1%; Score 125; DB 2; Length 1025; 17.5%; Pred. No. 2.4; ive 84; Mismatches 207; Indels 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DWREKEAKDLIELVORRITYLONPKDCSK---ARKLVCN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 -DEILLDLGHHERS----
                                                                                                                                                                                     Best Local Similarity 17.5
Matches 105; Conservative
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A;Status: preliminary
                                                                                                              A; Map position: 1
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              synaptonemal complex protein - golden hamster (fragment)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Uul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: 148176
B;Dobson, M.J.; Pearlman, R.E.; Karaiskakis, A.; Spyropoulos, B.; Moens, P.B.
J;Cell Sci. 107, 2749-2760, 1994
A;Title: Synaptonemal complex proteins: occurrence, epitope mapping and chromosome disju
A;Reference number: 148176; MUID:95181577; PMID:7876343
A;Recession: 148176
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-845 <RES>
A;Coss-references: GB:L32978; NID:9598124; PIDN:AAC42039.1; PID:9598125
C;Genetics:
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C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Accession: H86250
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; C'Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowery, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Tilles-ear and analysis of chromosome I of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257 TVFRPVSETCTDRSGL--STGHWSGEVNDKNIQVVELPI-VDSLHPR-----PPYLPLAV 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484 NKSKYIEELHQENKALKKKSSAESKQLNAYEIKVNKLQLELESAKQKFQEMTDNYQKEIE 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEDLADRLIRVHGDPAVWWVSQFVKYLIRPQPWLEKEIE-EATKKLGFKHPVIGVHVRRT 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 845;
                                                                                                                                                                                                                                                                                                                                                                                                                          4.1%; Score 125.5; DB 2;
19.7%; Pred. No. 1.7;
trive 81; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 19.74
Matches 85; Conservative
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867
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Cispecies: Schizosaccharomyces pombe
Cispecies: Schizosaccharomyces pombe
Cispecies: Jun-2000 #sequence_revision 21-Jun-2000 #text_change 04-Feb-2000
Cispecession: T45527
Rijmenez, M.; Goday, C.
Rijmenez, M.; Goday, C.
Rijmenez, C.
Rijmenez, M.; Goday, C.
Rijmenez, M.; 
808 VEGKRAAKEEL()NRLGLKSADFPVVGIITRLTHQKGIHLIKHAIWRTLERNGQVVLLGSA
                                                                                                                                                                                 --VHVEEHFQLLARRMQV---DKKRVYLATDDPTLLKEAKTKYSNYEFISDNSISWSAGL
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Experimental source: strain 972h(-)
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Pred. No. 8.7;
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19.9%;
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Best Local Similarity
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OY 184AKDLTELVQRRITYLQNPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRT 240  136 LVSKENLIEELNQEIGHLKSELETVKSKSEDLENERAQNGSKI 1368  OY 241 LILESQNWRYATGGMETVFRPVSETCTDRSGLSTGHWSGEVNDKNIQVVELPIVDSLHPR 300  1369 EQLELKNTKLA-AAMRTKYEQVVNKSLEKHNQIRQQLSQKTSELEAKVAECHQLNEQLNK 1427  OY 301 PPYLLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEBATKKLGFKHPVI 360  1428 PSATFTATTQSEPSTVSLEEFNSTKEELSSTQRKLSEIMDIL 1469  OY 361 GVHVRRTDKVGTEAAFH-PIEEYMTKEELSSTQRKLSEIMDIL 1469  OY 362 GVHVRRTDKVGTEAAFH-PIEEYMTKEELSSTQRKLSEIMDIL 1469  OY 363 GVHVRRTDKVGTEAAFH-PIEEYMTKEELSSTQRKLSEIMDIL 1529  OY 408 TDDPTLLKEAKTKYSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHF 456  DD 1530 KQNQVLQDQVKALQETVVSSEEAASSAVHADTKDLENLKKTEEMLSVTFQVIFNESISDF 1589  OY 457 -LSQADFLVCTFSSQVCRVAYEIMQTLHPDASANFHSLDDI 496  1590 STSTRADFTTFVQKEWEKRREILGKDVBEGVAQSHQKQLDNI 1630	SSULT 8  Golds  OOS.10 procein - Arabidopsis thaliana  OOS.10 procein - Arabidopsis thaliana (mouse-ear cress)  Species Arabidopsis thaliana (mouse-ear cress)  Date: Arabidopsis thaliana (mouse-ear cress)  Date: Arabidopsis thaliana (mouse-ear cress)  Accession: F86161  Theologis, A.; Eker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White  Min, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.;  Theologis, A.; Eker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White  Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Maiti,  Authors: Salzberg, B.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun,  T., M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  Reference number: A86141; MUID:21016719; PMID:11130712  Accession: P86101  Residues: 1-174 csTO>  Ouery Match  Bestidues: 1-174 csTO>  Ouery Match  As Davis, M.; Manatches 225; Indels 224; Gaps  AS HPDHSRREISKILAKLERIKQONEDLRRMA-ESLRIPEOFIDGG	Qy 211 VCNINKGCGYGCQLHHVVYCFMIAYGTQ
Matches   104;   Conservative   78;   Mismatches   223;   Indels   118;   Gaps   19;	OY 361 GUNTREDKY	

Db 839 QFSESRMNGMESTIHHLQDENQCRVREYQVELDRAHDAHIEIIVLQKCLQDWLEKSSSLI 898	Qy 185 KDLTELVQR 193
Oy 243 LESQNWRYATGGWETVFRPVSETCTDRSGLSTGHW277	Db 1234 EEAAAVVSR 1242
899 AENODIKEASKLLEKLVSELEEENIGKQVQIDSSINCIKILRTGIYQVLMKLEIIPG	RESULT 10
QY 278SGEVNDRAIQVVELPIVDSLHPRPPYLPLAVPEDLADRILRVHGDPAVWWVSQ 330        :	T30934 myosin-like protein - Parascaris univalens C.Snecies: Parascaris univalens
331 FUKYITRDODMIRKRIRBATKKIGRKHDVIGUNRRTDKVGTRARHDI 379	C. Species: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000 C. Accession: T10914
1003 FLRQLKSEAVG	
JARRMQVDKKRVYLATDDPTLL	A; Title: PUMA1: a novel protein that associates with the centrosomes, spindle and centro A; Reference number: Z20936; MUID:98139561; PMID:9472001
Db 1063LMVEIEDFHRQVLQLRDDYTILQGDNNKTLDEKAYL-TKSTLQLEEEKCKLED 1114	A;Accession: 199334 A;Actus: primary; translated from GB/EMBL/DDBJ a:Molecule tyme: mpNa
QY 429 DNSISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIMQ 480	A; Rosidues: 1-1955 < EBET.> A; Cross-references: EMBL: AF009623; NID: g3068589; PID: g3068590; PIDN: AAC38995.1 C; Genetics:
481	
	Query Match 3 8%; Score 117; DB 2; Length 1955; Best Local Similarity 19:6%; Pred. NO. 20; Matches 94; Conservative 80; Mismatches 181; Indels 124; Gaps 23;
534 NHWDGYSKGINRKLGKTGLYPSYKVREKIE 563	41 RELSKILAKLERLKOONEDLRRMAESLRIPEGPIDQGTATGRVRVLEEQLVKA 9
Db 1230 NEKSELSKAVEGLECRYKEAKAIE 1253	DD 788 RDLKDAMTEVEELKKQLQKMDEENSERLESVLRTKISSDTVDTSBIAEYTEVKV 841
RESULT 9	Qy 94 KEQIENYKKQARNGLGKDHEILRRRIENGAKELWFFLQSELKKLKHLEGNEL 145
proble heat shock protein, 53413-59028 [imported] - Arabidopsis thaliana	ILEDELAERQRIVERQRTEMN
C;Species: Arabidopsis thaliana (mouse-ear cress) C;Dart=001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accesion: Decide	Qy 146QRHADEILLDIGHHERSIMTDLYXLSQTDGAGDWREKEAKDLTELVQRRITYLQN 200
C.A.Cession: D90,90 R;Theologis A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin. C.W.: Chung, M.K.: Conn. L.: Conwav. A.B.: Conwav, A.R.: Creasy, T.H.: Dewar, K.;	DD 893 EYQLESDRIRAEMATVELKYQSEVEDERDQRSRDADSWKVTSEELRSKISFWEK 946
	OY 201 PKDCSKARKLVÇNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQN 247 : :    :   :   :   :
A. Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,	Db 947 MLEEAKHRETVLREEATEWEEKHDIISNESLKLRNEIERIRSDAEEDIQK 996
Ξ.	248 WRYATGGWETVFRPVSETC-TDRSGLSTGHWSGEVNDKNIQVVELPIVDSLHPRP
	Db 997 WKKDVHMAQNELKNLERVCETLRSQLTAANDRVASLNTTINEQTSKIRELNSHEH- 1051
A;Reference number: A86141; MUID:21016719; PMID:11130712 A;Accession: D96796	302 PYLPLAVPEDLAURLLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPV :
A;Status: preliminary A;Molecule type: DNA	
A;Residues: 1-1871 <sto> A;Cross-references: GB:AE005173; NID:g6143906; PIDN:AAF04452.1; GSPDB:GN00141 C;Genetics:</sto>	Qy 360 IGVHVRRTDKW;TEAAFHPIEEYMVHVEEHFQLLARRMQVDKKRVYLATDDPTLLKEAKT 419
A;Gene: F28016.15 A;Map position: 1	Qy 420 KYSNYBPISDNSISWSAGLHNRYTENSLRGVILDIHPLSQADFLVCTFSSQVCRVAYEI 478
cal Similarity 23.8%; Pred. No. 19;	Db 1140 KIEKLRIEHDHLERDYREKTKEVDRLKEVEKTFELKVNRARQEL 1183
Matches 45; Conservative 38; Mismatches 76; Indels 30; Gaps	RESULT 11
QY 24 YIGGHLVRDNDHPDHSSERLSK-ILAKLEKLKQQNEDLRRMAESLKIPEGFIDQSIATGK 82	B/12/65 hypothetical protein APE0110 - Aeropyrum pernix (strain K1) C.Species: Aerobyrum pernix
83 VRVI.EEOLVKAKEOIENYKKOARNGI.GKDHEILIRRRIENGAKEIWF 128	C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 02-Feb-2001 C;Accession: B72765
	R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takaniya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K pan post coloring to the control of th
129 FLQSELKKLKHLEGNELQRHADBILLDLGHHERSIMTDLYYLSQTDGAGDWREKEA 184	A,Title: C, Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy: A,Reference number: A72450; MUID:99310339; PMID:10382966
Db 1175 -VETEISDHKEKVKKKDEDYILRSQDTGKVDLGERERRSKQRKIHKSVEDEIGDQEDEDA 1233	A;Accession: B72765 A;Status: preliminary

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Cross-references: EMBL:X08067; NID:g6798; PIDN:CAA30856.1; PID:g6799
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                                                              myo-3; CESP:K12F2.1
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A,Reference number: S02771
A,Status: nucleic acid sequence not shown
A,Nolecule type: DNA
A,Residues: 1-116,140-1992 <DIB>
           A;Molecule type: DNA
A;Residues: 1-919 < KAMA
A;Residues: 1-919 < KAMA
A;Cross-references: DDBJ:AP000058; NID:g5103388; PIDN:BAA79020.1; PID:g5103499
A;Experimental source: strain K1
C;Genetics:
A;Gene: AFDG110
C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032
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R; Harris, B.
Submitted to the EMBL Data Library, August 1996
A; Reference number: Z19773
A; Reference number: Z19773
A; Accession: T23622
A; Accession: T2362
A; Accession: T362
A; Acc
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N;Contains: myosin ATPase (EC 3.6.4.1)
C;Species: Caenorhabditis elegans
C;Date: 31-Dec-1993 #sequoce_revision 19-May-2000 #text_change 19-Apr-2002
C;Accession: T23622; 802771
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                                                                                                                                                                                                                                         Length 919;
                                                                                                                                                                                                                                                                                              70; Mismatches 160;
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692 E----AEEKKLRKEVSRKSEIEARLKEV-
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Matches 108; Conserv
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Dystrein C18H9.8 [imported] - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Species: O-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: H88187
R;Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Title: Genome sequence of the newatode C. elegans a platform for investigating biolog A;Title: Genome websites genome.wustl.edu/gsc/C_elegans/ and www_manger.ac.uk/Projects/C_elegans/A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: H88187
                                                                                                 methylated amino acid; muscle
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KLSDITGQLEDMQERNEDLARQKKKTDQELSDTKKHVQDLELSLRKAEQEKQSRDHNIRS 1013
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A;Molecule type: DNA
A;Redidues: 1-678 <STO>
A;Cross-references: GB:chr_II; PID:g722387; GSPDB:GN00020; CESP:C18H9.8
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEEQLVKAKEQIENYKKQARNGLGKDHEILRRRIENGAKELWFFLQSELKKLKHLE-
                                                                                                                                                                                                                                                                                                                                                         F;1190-1992/Region: light meromyosin
F;133/Modified site. N6,N6,N6-trimethyllysine (Lys) #status predicted
F;208/Binding site: ATP (Lys) #status predicted
F;208/Binding site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVIGVHV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRSRQDLEKALKTIEVQYSELQTKADEQSRQLQDFAALKNRLNNENS 1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T------LLKEAKTKYSNYEFISD---NSISWSAGLHNRY-TENS 446
                                                            homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKVAQENIDEİTK------ÖKHDV------
                      Aintrons: 46/1; 192/1; 468/2; 1921/3
C; Superfamily: myosin heavy chain; myosin motor domain ho C; Superfamily: myosin heavy chain; myosin motor domain horords: myosin motor domain homology colled coil; hydrolase; ng 18,202-209/Region: myosin motor domain homology cMMOT>
F; 202-209/Region: actin binding #status predicted F; 93-807/Region: actin binding #status predicted F; 93-807/Region: actin binding #status predicted F; 975-1992/Domain: coiled coil #status predicted col>
F; 875-1189/Region: S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 116.5; D
Pred. No. 23;
59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 ELSKILAKLERLKQQNEDLRRMAE-----
A,Map position: 5
A,Introns: 46/1; 192/1; 292/1; 468/2; 1921/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|:: ||: ||:
1062 KLEQQMDEL-----EENID------
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276 HWSGEVNDKNIQVVELPIVDSLHPRPPYLPL-----AVPEDLADRLLRVHGDPAVWWVS 329
                                                                                                                                                                                                                                                        330 QFVKYLIRPQPWLBKEIBEATK------KLGFKHPVIGVHVRRTDKVGTEAA 375
                                                                                                                                                                                                                                                                                                 EREEQLIKAKEKLENDIAEIMKMSGDNSSQLTKOMNDELRLKERDVEELQLKLTKANENAS 962
                                                                                                                                                                                                                                                                                                                                                    F--HPIEBYMVHVEEHFQLLARRMQVDKKRVYLATDDPTLLKEAKTKYSNYEFIS---DN 430
                                                                                                                                                                                                                                                                                                                                                                                                                                              SISWSAGLHNRY-----TENSLR-----GVILDIHFL-SQADFLVCTFSSQVC 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRVRVLEEQLVKAKEQIENYKKQARNGLGK-DHEILRRRIENGAKELWFFLQSELKKLKH 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKEAKDLTELVORRITYLONPKDCSKARKLVCNINKGCGYGCOLHHVVYCFMIAYGTORT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LILESQNWRYATGGWETVFRPVSET--CTDRSGLSTGHWSGEVNDKNIQVVELPIVDSLH 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LV--EPKWACAT---EECFKNIANNFLCCSQEDAATLR-----KIFDILKIPSND--- 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRPPYLPLAVFEDLADRLLRVHGDPAVWWVSQF--VKYLIRPQPWLEKEIEEATKKLGFK 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-1137 <WIL>
A;Cross-references: EMBL:278416; PIDN:CAB01681.1; GSPDB:GN00028; CESP:C23H4.6
A;Experimental source: clone C23H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C23H4.6 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                    216 KGCGYGCQLHHVVYCFMIAYGTQRTLILESQNWRYATGGWETVFRPVSETCTDRSGLSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---ERLKQQNEDLRRMAESLRIPEGPIDQGTAT
                                                                                                                                                                                                       -----VNKLHOKEEOFNMLSSDLEKLRENLADMEAKFREK---
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Pred. No. 13;
5; Mismatches 156; Indels 134;
                                                                                                      ENLSEVSQVKE'TL-----EKELQILKEKFARASEBAVSVQRSMQET
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A;Molecule type: DNA
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A;Introns: 34/1; 76/1; 111/2; 482/2; 598/2; 1091/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R,Wilkinson, J.
submitted to the EMBL Data Library, August 1996
AFeference number: Z19121
A;Accession: T19414
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19.4%; Pred
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Best Local Similarity 19.4%
Matches 88; Conservative
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C; Accession: T19414
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C.Species: Homo sapiens (man)
C.Species: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 05-Nov-1999
C.Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 05-Nov-1999
C.Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 05-Nov-1999
C.Accession: S25655, 379853
B.Bibb, G., Delabie, J.; Brueggen, J.; Richener, H.; Asselbergs, F.A.M.; Cerletti, N.;
EMBO J. 11, 2103-213, 1992
B.A.Title: Restin: a novel intermediate filament-associated protein highly expressed in the A.Title: Restin: a novel intermediate filament-associated protein highly expressed in the A.M. A.Molecule type: mRNA
A.M. Residues: 1-1477 **ALL>
A.K. Residues: 1-1477 **ALL>
A.K. Residues: 1-1477 **ALL>
A.K. CASS **REFERENCE** EMBI:X64838; NID:G35998; PIDN:CAA46050.1; PID:G35999
C; Keywords: cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 YYLSQTDGAGDWREKEAKDLTELVQRRITYLQNPK--DCSKARKL------VCNIN 215
                                                                                                                                                                                                                                                                                                                                                       ---HLEGNELORHA---DEILLDLGHHERSIMTDLYYLSQTDGAGDWREKEAKDLTELVQ 192
                                                                                                                                                                                                                                                                                                                                                                                    YEIEIRSNPLKKKAIQLQETLDTLKKQEEKLMEDMQSALTPEA---WRDKMSENMKQLNA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----NIQVVELPI----VDSLHPRPPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 YLIRPOPWLEKEIEEATKKLGFKHPVIGVHVRRTDK--VGTEAAFHPIEEYMVHVEEHFQ 391
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                                                                                                                                                                                                  | || || EEQKKL------NEAVTHAMDPQMKEKYEDLKSEAKLLKERVVEMEAKNEDLDDRISK
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                                                                                                                                                                38 HSSRELSKILAKLERLKQQNEDLRRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQI
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                                                                                                                    81; Mismatches 185; Indels 122;
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                                                                      ; DB 2;
5.6;
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                                                                      Score 116;
Pred. No. 5
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                                                                         Query Match 3.8%;
Best Local Similarity 18.1%;
Matches 86; Conservative 8
  A;Gene: C18H9.8
A;Map position:
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Db 560 -RPTIV	Db 629PKYAVKAYTPDASGIFANGLHSGYRFYSSRG 659 Search completed: February 2, 2004, 08:43:58
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OM protein - protein search, using sw model

February 2, 2004, 08:39:39; Search time 10:5 Seconds (without alignments) 2575.272 Million cell updates/sec Run on:

US-09-971-773-24 3085 1 MRAWIGSWRWIMLILFAWGT......XKVREKIETVKYPTYPBAEK 575

Title: Perfect score:

Scoring table: Sequence:

127863 seqs, 47026705 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	E	Q9byc5 h alpha-(1,	Д	Ø		_	Q9vjd3 drosophila	bos		schiz	O61308 parascaris		caenc	homo	рошо	sulfc		rattı		xenor		homo	8 mus m	P12883 homo sapien	ratt	mus	'n		Q99ur5 staphylococ	m	-	2420 mus mus	Q43846 solanum tub
SUMMARIES	ID	FUT8 MOUSE	FUT8 HUMAN	FUT8_BOVIN	FUT8_PIG	SCP1_RAT			MYHA_BOVIN		ALM1_SCHPO	PUMA PARUN	RASO_AERPE	MYSA CAEEL	REST_HUMAN	OSF1_HUMAN	RA50_SULTO	CARB_STAAW	ITNI_RAT	CENF_HUMAN	ITN1_XENLA	NEBL_HUMAN	DYNA_HUMAN	DYNA_MOUSE	MYH7_HUMAN	MYH9 RAT	SCP1 MOUSE	CTRO MOUSE		CARB STAAM	DYNA_RAT	MYH7_RAT	SH32_MOUSE	UGS4_SOLTU
	DB	-	Н	П	7	Н	Н	Н	-	-	н	н	н	н	н	-	Н	Н	Н	Н	7	-	Н	Н	-		М	~	Н	Н	Н	Н	Н	Н
	Length	575	575	575	575	997	845	751	1976	916	1727	1955	919	1969	1427	214	879	1057	1217	3210	1270	1014	1278	1281	1935	1961	993	1597	978	1057	1280	1935	352	1230
ď	Query Match	9.66	97.3	96.0	94.3	4.1	•	3.9	3.9	3.8	3.8	3.8	3.8	3.8	3.7	3.7	3.7	3.7	3.7	3.7	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.5	3.5	3.5
	Score	3074	3003	2961	2910	126	125.5	120.5	119.5	118.5	118	117	116.5	116.5	115.5	114	113	113	113	113	112.5	112	111.5	111.5	111.5	111.5	111	111	110.5	110	110	109.5	109	109
	Result No.		7	m	4	ß	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P13540 mesocricetu Q9uzce pyrococcus P16019 theileria a P15619 theileria a P15580 homo sapien Q9z67 chlamydia p Q9z67 chlamydia p Q9z67 mus musculu P79293 sus suscrofa Q08378 homo sapien Q14578 homo sapien Q20060 caenorhabdi Q9y623 homo sapien
MYH7 MESAU RASO_PYRAB HS70_THEAN MYH4 HUWAN RWUC_CHLPN TITML MOUSE MYH7_PIG G160_HUWAN TPR HUWAN TPR HUWAN SWG-CABEL
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109 107.5 107.5 107.5 107 107 106.5 106.5 106.5
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## ALIGNMENTS

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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Taniguchi N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taniguchi N.
                    481
                                                                                                                                                     RESULT 2
FUT8_HUMAN
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                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIENYKKQARNGLGKDHEILRRRIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGAKELWFFLQSELKKLKHLEGNELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGDWR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVI 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSNYBFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYBIMQ 480
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glucosaminyl-(1->2)-alpha-D-mannosyl-(1->6)}-beta-D-mannosyl-(1->4)-N-acetyl-beta-D-glucosaminyl-(1->4) [alpha-L-fucosyl-(1->6)}-N-acetyl-beta-D-glucosaminyl-(1->4) [alpha-L-fucosyl-(1->6)}-1-PATHWAX: Glycosylation.
-!-PATHWAX: Glycosylation.
-!-SUBCELLULAR LOCATION: Type II membrane protein. Membrane-bound form in trans cisternee of Golgi (By similarity).
-!-SIMILARITY: CONTEINS 1 SH3 domain.
-!-SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVNDKNIQVVELPIVDSLHPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVNDKNIQVVELPIVDSLHPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVHVRRTDKVGTEAAFHPIEEYMVHVEEHFQLLARRMQVDKKRVYLATDDPTLLKEAKTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKEAKDLTELVQRRITYLQNPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRT
                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMPORTANT FOR DONOR-SUBSTRATE BINDING.
T -> S (IN REF. 2).
Q -> E (IN REF. 2).
N -> K (IN REF. 2).
                                                                                                                                                                                                                                                                                              InterPro; IPR00145; SH3.
Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
PROSITE; PSS0002; SH3; PALSE_NEG.
Transferase; Glycosyltransferase; Transmembrane; Signal-anchor; Golgi stack; SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.6%; Score 3074; DB 1; Length 575; 99.5%; Pred. No. 6.9e-203; ive 2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
LUMENAL, CATALYTIC (POTENTIAL)
SH3.
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                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                      EMBL; AB025198; BAA76392.1; -. EMBL; BC010666; AAH10666.1; -.
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Best Local Similarity 99.5
Marches 572; Conservative
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575 AA;
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DOMAIN
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CONFLICT
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-!- FUNCTION: Catalyzes the addition of fucose in alpha 1-6 linkage to the first GloNAc residue, next to the peptide chains in N-glycans.
-!- CATALYTIC ACTIVITY: GDP-L-fucose + N(4)-{N-acety1-beta-D-glucosaminy1-(1->2)-alpha-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-beta-D-mannosy1-(1->6)-
                                                                  TLHPDASANFHSLDDIYYFGGQNAHNQIAVYPHKPRTEEEIPMEPGDIIGVAGNHWDGYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUTB_HUMAN STANDARD; PRT; 575 AA.

Q9BYG5; O00235; Q9BYC6; Q9P2U6;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
41pha-(1,6)-fucosyltransferase (EC 2.4.1.68) (Glycoprotein 6-alpha-L-fucosyltransferase) (GDP-fucose-glycoprotein fucosyltransferase)
(GDP-L-FDC:N-acceyl-beca-D-glucosaminide alpha1,6-fucosyltransferase)
(alpha1-6FUCT) (Fucosyltransferase 8).
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J. Biochem. 121:626-632(1997).
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SUBCELLULAR LOCATION: Type II membrane protein. Membrane-bound form in trans cisternae of Golgi (By similarity).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sasho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DONOR SUBSTRATE BINDING, AND MUTAGENESIS OF ARG-365 AND ARG-366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cailleau A., Balanzino L., Candelier J.J., Oriol R., Mollicone "Differential splice variants of human FUT8 embryonic CDNA."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20229550; PubMed=10764839;
Takahashi T., Ikeda Y., Tateishi A., Yamaguchi Y., Ishikawa M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOPORMS 1 AND 2).
MEDLINE=20275614; PubMed=10814706;
Yamaguchi Y., Ikeda Y., Takahashi T., Ihara H., Tanaka T., S
Uozumi N., Yanagidani S., Inoue S., Fujii J., Taniguchi N.;
"Genomi C structure and promoter analysis of the human
alpha, 6-fucosyltransferase gene (FUT8):";
Glycobiology 10:637-643(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yanaqidani S., Uozumi N., Ihara Y., Miyoshi E., Yamaguchi
                                                                                                                                                                                                                                           575
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                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1), AND FUNCTION.
MEDLINE=97279058; PubMed=9133635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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300 360 360 420 420

480 540 540

480

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361 GVHVRRTDKVGTEAAFHPIEEYMVHVEEHFQLLARRMQVDKKRVYLATDDPSLLKEAKTK
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28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-(1,6)-fucosyltransferase (EC 2.4.1.68) (Glycoprotein 6-alpha-L-fucosyltransferase) (GDP-fucosyltransferase) (GDP-fucosyltransferase) (GDP-fucosminide alpha1,6-fucosyltransferase) (alpha1-6FucI) (Fuccsyltransferase 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha6-fucosyltransferase family.";
Mol. Biol. Bvol. 17:1661-1672(2000).
-!- FUNCTION: Catalyzes the addition of fucose in alpha 1-6 linkage to
the first Glonar residue, next to the peptide chains in N-glycans
                        EKEAKDLTELVQRRITYLQNPKDCSKAKKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRT
                                                                              LILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVNDKNIQVVELPIVDSLHPR
                                                                                                                                                                 PPYLPLAVPEDLADRILLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVI
                                                                                                                                                                                                                                                GVHVRRTDKVGTEAAFHPIEEYMVHVEEHFQLLARRMQVDKKRVYLATDDPTLLKEAKTK
                                                                                                                                                                                                                                                                                                                                     YSNYEFISDNEISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIMQ
                                                                                                                                                                                                                                                                                                                                                                        YPNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIMQ
                                                                                                                                                                                                                                                                                                                                                                                                                      TLHPDASANFHSLDD1YYFGGONAHNO1AVYPHKPRTEEE1PMEPGD1IGVAGNHWDGYS
EKEAKDLTELVQRR1TYLQNPKDCSKARKLVCN1NKGCGYGCQLHHVVYCFM1AYGTQRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type II membrane protein. Membrane-bound form in trans cisternae of Golgi (By similarity). TISSUE SPECIFICITY: Highest expression found in brain. Also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54)-N-acetyl-beta-D-glucosaminyl-(1-54)-N-acetyl-beta-D-glucosaminyl)asparagine = GDP + N(4)-{N-acetyl-beta-D-glucosaminyl-(1-52)-alpha-D-mannosyl-(1-53)-[N-acetyl-beta-D-glucosaminyl-(1-52)-alpha-D-mannosyl-(1-56)]-beta-D-mannosyl-(1-54)-N-acetyl-beta-D-glucosaminyl-(1-54)-[alpha-L-fucosyl-(1-54)-N-acetyl-beta-D-glucosaminyl-(1-54)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-64)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-64)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-64)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-64)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosaminyl-(1-56)-[alpha-L-fucosyl-(1-56)]-N-acetyl-beta-D-glucosamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: GDP-L-fucose + N(4)-{N-acetyl-beta-D-glucosaminyl-(1->2)-alpha-D-mannosyl-(1->3)-[N-acetyl-beta-D-glucosaminyl-(1->2)-alpha-D-mannosyl-(1->6)}-beta-D-mannosyl-(1-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Lung;
MEDLINE=20523969; PubMed=11070054;
MEDLINE=20523969; PubMed=11070054;
Javaud C., Dupuy F., Maftah A., Michalski J.-C., Oriol R.,
Petit J.-M., Julien R.; Free of FUTS; the gene encoding the
"Annestral exonic organization of FUTS; the gene encoding the
alpha6-fucosyltraneferase, reveals successive peptide domains
suggest a particular three-dimensional core structure for the
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                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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BURGHTANT FOR DONOR SUBSTRATE BINDING.

BURDKANQVVULE-BUDSLHPREPYLELANPEDLADBLURVH

GDPAVWWVS -> TPIMNLLVITLFPGQLDCTIDTQKIHFV
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Transferame; Glycosyltransferame; Transmembrane; Signal-anchor;
Golgi stack; SH3 domain; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E (in isoform 2).
/Frid=vSP 001807.
missing (in isoform 2).
Frid=vSP 001808.
R->A,K: COMPLETE LOSS OF ACTIVITY.
R->A,K: DEGREASES ACTIVITY TO 38.
                                name_1 isoid=Q9BXCS-1; Sequence=Displayed; Name=2; Synonyms=Retinal; Name=2; Synonyms=Retinal; Isoid=Q9BXCS-2; Sequence=VSP_001807, VSP_001808; SIMILARITY: Contains 1 SH3 domain. SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMÎC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LUMENAL, CATALYTIC (POTENTIAL).
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splicing; Named isoforms=2;
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; Pred. No. 5e-198;
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB049828; BAB40975.1; -. AB0493740; BAB40229.2; -. AB032573; BAA928589.1; -. AB032572; BAA92858.1; -. AB032569; BAA92858.1; JOINED. AB032570; BAA92858.1; JOINED. AB032571; BAA92858.1; JOINED. AB032571; BAA92858.1; JOINED.
                                                                                                                                                                                                                                                                                                                                   D89289; BAA19764.1; -. AF038281; AAB92372.2; -. AF038280; AAB92372.2; JOINED. Y17979; CAA76988.1; -.
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96.5%;
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Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
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575 AA;
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SEQUENCE
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Best Local Similarity
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28-FEB-2003
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ID FUT8 1
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                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRPWTGSWRWIMLILFAWGTLLFYIGGHLVRDNDHPDHSSRELSKILAKLERLKQQNEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLHPDASANFHSLDD1YYFGGONAHNQ1AVYPHKPRTEEE1PMEPGD11GVAGNHWDGYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGAKELWFFLQSELKKLKHLEGNELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGDWR
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                                                                                                                                                                                                                                                                                                                                                           SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                           EMBL; AF247186; AAF65460.1; -.
InterPro; IPR001452; SH3.
Pfam; PP00018; SH3; 1.
PROSITE; PS50002;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
in heart, lung, spleen and kidney.
SIMILARITY: Contains 1 SH3 domain.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.0%; Score 2961; DB 1; Length 575; 95.0%; Pred. No. 3.7e-195; ive 15; Mismatches 14; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                LUMENAL, CATALYTIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FE04C66B8A5BF540 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SH3-BINDING (POTENTIAL)
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Truncation and Cuba Cioning of potities Diain Observations and Cuba Alphal-->6 fucosyltransferase.";

The beta-D-glucosaminde alphal-->6 fucosyltransferase.";

L. Biol. Chem. 271:27810-27817(1996).

The first GlorAc residue, next to the peptide chains in N-glycans.

C. FUNCTION: Catalyzes the addition of fucose in alpha 1-6 linkage to the pitst GlorAc residue, next to the peptide chains in N-glycans.

C. CATALYTIC ACTIVITY: GDP-L-fucose + N(4) - {N-acetyl-beta-D-glucosaminyl-(1-x2)-alpha-D-mannosyl-(1-x3)-[N-acetyl-beta-D-glucosaminyl-(1-x3)-[N-acetyl-beta-D-glucosaminyl-(1-x3)-alpha-D-mannosyl-(1-x6)]-beta-D-glucosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-beta-D-glucosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-beta-D-glucosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-beta-D-glucosaminyl-(1-x6)]-beta-D-mannosyl-(1-x6)]-beta-D-glucosaminyl-(1-x4)-{alpha-L-fucosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-beta-D-glucosaminyl-(1-x4)-{alpha-L-fucosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x2)-alpha-D-mannosyl-(1-x6)]-contosaminyl-(1-x6)-(1-x6)]-contosaminyl-(1-x6)-(1-x6)-(1-x6)-(1-x6)-(1-x6)-(1-x6)-(1-x6)
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                                                                                                                           28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-(1,6)-fucosyltransferase (EC 2.4.1.68) (Glycoprotein 6-alpha-L-fucosyltransferase) (GDP-fucose--glycoprotein fucosyltransferase) (GDP-L-Puc:N-acetyl-beta-D-glucosaminide alpha1,6-fucosyltransferase) (alpha1-6FucT) (Fucosyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97066976; PubMed=8910378; Uozumi N., Yanagidani S., Miyoshi E., Ihara Y., Sakuma T., Gao C.-X., Uozumi N., Yanagidani S., Shiba T., Taniguchi N.; "Pujii S., Shiba T., Taniguchi N.; "Purification and cDNA cloning of porcine brain GDP-L-Fuc:N-acetyl-"Purification and cDNA cloning of porcine brain GDP-L-Fuc:N-acetyl-
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metāzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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Transferase; Glycosyltransferase; Transmembrane; Signal-anchor;
Golgi stack; SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., SEQUENCE OF 102-130; 333-344; 402-415 AND 566-575, AND FUNCTION.
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LUMENAL, CATALYTIC (POTENTIAL).
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Pred. No. 1.1e-191;
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InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
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EMBO J. 11:5091-5100(1992).
-!- FUNCTION: MAJOR COMPONENT OF THE TRANSVERSE FILAMENTS OF
SYNAPTONEMAL. COMPLEXES (SCS), FORNED BETWEEN HOMOLOGOUS
CHROMOSOMES DURING MEIOTIC PROPHASE.
-!- SUBCELLULAR LOCATION: NUCLEAR. IN TRIPARTITE SEGMENTS OF
SYNAPTONEMAL. COMPLEXES, BETWEEN LATERAL ELEMENTS IN THE NUCLEUS.
FOUND ONLY WHERE THE CHROMOSOME CORES ARE SYNAPSED. ITS N-TERMINUS
IS FOUND TOWARDS THE CENTRE OF THE SYNAPTONEMAL COMPLEX WHILE THE
C-TERMINUS EXTENDS WELL INTO THE LATERAL DOMAIN OF THE
                                                                                        LALESHWWRYATGGWETVFRPVSETCTDRSGSSTGHWSGEVKDKNVQVVELPIVDSVHPR
                                                                                                                                                                                                                                                                                     PPYLPLAVPEDLADRIVRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVI
                                                                                                                                                                                                                                                                                                                                       GVHVRRTDKVGAEAAFHPIEEYTVHVEEDFQLLARRMQVDKKRVYLATDDPALLKEAKTK
                                                                                                                                                                                                                                                                                                                                                                                      421 YPSYEFISDNSISWSAGLHNRYTENSLRGVILDIHFILSQADFLVCTFSSQVCRVAYEIMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                      ALHPDASANFRSLDDIYYFGGPNAHNQIAIYPHQPRTEGEIPWEPGDIIGVAGNHWDGYP
                        MRAWTGSWRWIMLILFAWGTLLFYIGGHLVRDNDHPDHSSRELSKILAKLERLKOONEDL
                                      MR PWTGSWRWIML ILFAWGTLLFYIGGHIVRDNDHSDHSSRELSKILAKLERLKQONEDL
                                                                       RRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIENYKKQARNGLGKDHEILRRRIE
                                                                                                                        NGAKELWFFLQSELKKLKHLEGNELORHADEILLDLGHHERSIMTDLYYLSQTDGAGDWR
                                                                                                                                               121 NGAKELWFFLQSELKKLKNLEGNELQRHADEFLSDLGHHERSIMTDLYYLSQTDGAGDWR
                                                                                                                                                                        EKEAKDLTELVORR I TYLONPKDCSKARKLVCN I NKGCGYGCOLHHVVY CFM I AYGTORT
                                                                                                                                                                                                                       LILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVNDKNIQVVELPIVDSLHPR
                                                                                                                                                                                                                                                                        PPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVI
                                                                                                                                                                                                                                                                                                                         GVHVRRTDKVGTEAAFHPIEEYMVHVEEHFQLLARRMQVDKKRVYLATDDPTLLKEAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                        TLHPDASANFHSLDDIYYFGGONAHNOIAVYPHKPRTEEEIPMEPGDIIGVAGNHWDGYS
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lersel M., Heyting C.;
"A coiled-coil related protein specific for synapsed regions
23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGINRKLGKTGLYPSYKVREKIETVKYPTYPEARK 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994 (Rel. 29, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sycaptronemal complex protein 1 (SCP-1 protein)
SYCP1 OR SCP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             997 AA
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Testis;
MEDLINE-93099884; PubMed-1464329;
 14;
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
  538;
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Q03410;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------HFQLLARR---MQVDKKRVYLATDDPTLLKEAKTKYSNYEFISDNSISWSA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 KKQ------ARNGLGK---DHEILRRRIENGAKELWFFLOSELKKLKHLEGNELOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::
EYEREETRQVY'VDLMNNIEKMILAFEELRVQAENARLEMHFKLKEDHEKIQHLE-BEYQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 HAD-----EILLDLGHHERSIMTDLYYL--SQTDGAGDWREKEAKDLTELVQRRITYLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKSSELEEMTKFRONNKEVELEELKTI - - - - - LAEDQKLLDEKKQVEKLAEELQGKEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     505 TELEKEKLKNIELTANSDMLILENKKLVQEASDMVLELKKHQEDIINCKKQEERMLKQIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | |: || |: || |: || |: || ENEKVSLKLEFEIQENKDL------IKENNATRHWCNLLKETCARSAEKTSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 NPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQNWRYATGGWETVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316 EKKOHLTS-----ELEDIKMSMQRSMSTQKTL---EEDLQIAT---KTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLTEEKEAQMEELNKAKTTHSLVVTELKATTCTLEELIRTEQQRLENNEDQLKLITMELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KNIQVVELPIVDSLHPRPPYLPLAVPEDLADRLLRVHG-DPAVWWVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELSKILAKLERLKQQNEDLRRMAESLRIPEGPIDQGTATGR-VRVLEEQLVKAKEQIENY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL). (POTENTIAL). (POTENTIAL).
TISSUE SPECIFICITY: Testis.
DEVELOPMENTAL STAGE: EXPRESSED EXCLUSIVELY IN MEIOTIC PROPHASE
                                                                                                       C-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLHNRYTENSLRGVILDI - - HFLSQADFLVCTF - - SSQVCR - VAYEIMQ 480
                                                                                              FLANKED BY N- AND C-TERMINAL GLOBULAR DOMAINS. THE C-TER DOMAIN HAS DNA-RINDING CAPACITY.
CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT CORRECTED IN POSITION 6 TO MAXIMIZE THE SIMILARITY WITH OTHER SPECIES SYCPI SEQUENCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 997;
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                                                                              DOMAIN: CONSISTS OF AN ALPHA-HELICAL STRETCH OF 700 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               905 NUCLEAR LOCALIZATION SIGNAL
990 ARG/LYS-RICH (BASIC)
116511 MW; 229D59823FD684BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, X67805, CAA48006.1, ALT FRAME.
Nuclear protein, Majosis, Cell division, Phosphorylation,
DNA-binding, Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEAR LOCALIZATION SIGNAL NUCLEAR LOCALIZATION SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 0.65; 78; Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ź
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        997 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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DOMAIN
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    COGS_DROME (09VJD3; 08T0G3; 28-FEB-2003 (Re.
                                                                                                                                                                                                                                                                                                                                         FWS OR CG6549.
                                                                                                                                                                                                                                                                                         28-FEB-2003
15-SEP-2003
                                                                                                                                                             409
                                                          309
                                                                                                            368
                                                                                                                                    969
                                                                                                                                                                                     959
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                                                                                                                                                                                                                                        COGS_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 YKKQARNGLGKDHEILRRRIENGAKELWFFLQSELKKLKH--------LEGNELQRH 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELSKILAKLERLKOONEDLRRMAESLRIPEGPID--OGTATGRVRVLEEQLVKAKEQIEN 99
                                                                                                                                                                                                                                                 GELI SGI. 107:271-2716 (1994).

-1- FUNCTION: MAJOR COMPONENT OF THE TRANSVERSE FILAMENTS OF SYNAPTONEMAL COMPENEXES (SCS), FORMED BETWEEN HOMOLOGOUS CHROMOSOMES DURING MEIOTIC PROPHASE (BY SIMILARIY). HAS NON-SPECIFIC DNA BINDING CAPABILITY.

-1- SUBCELLULAR LOCATION: NUCLEAR. IN TRIPARTITE SEGMENTS OF SYNAPTONEMAL COMPLEXES, BETWEEN LATERAL ELEMENTS IN THE NUCLEUS. FOUND ONLY WHERE THE CHROMOSOME CORES ARE SYNAPSED. ITS N-TERMINUS IS FOUND TOWARDS THE CENTRE OF THE SYNAPTONEMAL COMPLEX WHILE THE C-TERMINUS EXTENDS WELL INTO THE LATERAL DOMAIN OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 ADEILLDLGHHERSIMT----DLYYLSQTDGAGDWREKEAKDLTELVQRRITYLQNPKDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQ--NWRYATGGWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                               SYNAPTONEMAL COMPLEX.

DOMAIN: CONSISTS OF AN ALPHA-HELICAL STRETCH OF 700 AA RESIDUES,
FLANKED BY N- AND C-TERMINAL GLOBULAR DOMAINS. THE C-TERMINAL
DOMAIN HAS DNA-BINDING CAPACITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL) (POTENTIAL)
     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-SOO1 (Rel. 40, Last annotation update)
Synaptonemal complex protein 1 (SCP-1 protein) (Meiotic chromosome synaptic protein) (Fragment).
                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                            'Synaptonemal complex proteins: occurrence, epitope mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.57;
81; Mismatches 161; Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 845;
                                                                                                                                                                                                   Dobson M.J., Pearlman R.E., Karaiskakis A., Spyropoulos B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEAR LOCALIZATION SIGNAL NUCLEAR LOCALIZATION SIGNAL ARG/LYS-RICH (BASIC).

D7F28873C824C6A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear protein; Meiosis; Cell division; Phosphorylation; DNA-binding; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.1%; Score 125.5;
                                                                                     (Golden hamster).
                                                                                                                                                                               TISSUE=Testis;
MEDLINE=95181577; PubMed=7876343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLDKSEENARSIECEVLK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99401 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 19.74
Matches 85; Conservative
                                                                                                                                                                                                                                           chromosome disjunction.
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756
838
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                                                                                     Mesocricetus auratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; 148176; 148176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  845 AA;
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                      NCBI_TaxID=10036;
                                                                          SCP1 OR SYN1.
                                                                                                                                                                                                                   Moens P.B.;
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RA MEDLINE-ZO194006; PUNDRGG10731132;

RA MEDLINE-ZO194006; PUNDRGG10731132;

RA MADLINE-ZO194006; PUNDRGG1073132;

RA AMDRINE-ZO194006; PUDR RA. GAIDLE R.F., GADAGE R.A., GAIDLE R.F., GADAGE R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA STUTON G.G., Workman J.R., Sandell M.D., Zhang Q., Chen L.X., Miklos G.L.G. Randron R.C., Bager, R.G., Champpe M., Pfelifer B.D., RA Briton R.C., Barker E.G., Helt G., Nahson C.R., Miklos G.L.G. RA Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C. Baldwin D. RA Ballar R.M., Basu A., Baxedale J., Baytartaroglu L., Beasley E.M., RA Borkova D., Botchan M.F., Bouck J., Broketein P., Botchar P., Botchan M.F., Bouck J., Broketein P., Brother P., Chandra I. RA Glery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P. R. Ghery J.M., Lolcher A., Deng E., Mays A.D., Dew I., Dietz S.M., RA Gerblos B., Delcher A., Deng B., Dourson M., Dugal-R.C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., RA Gong F., Gorrell J.H., Qu. Z., Gunn P., Harris M., Harvey D., Heiman T.J., Herrandez J.R., Houck J., Harvey D., Heiman T.J., Herrandez J.R., Houck J., Lai X., Harken D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Lei Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lasko P., Milahina N.V., Mobarry C., Morris J., Moberrei A., Ban H., Spier B., Spradling A.C., Saunders R.D., Suth M., Wang X., Randers R.D., Pollard J., Puri V., Remington K., Saunders R.D., Suth T., Wang X., Mang Z.-Y., Wassathan G., Punner C., Shon H., Shipe B.C., Spradling A.C., Saunders R.D., Suth M., Wang X., Shipe B.C., Spradling A.C., Sanner C., Was B., Zhu S., Zhu S., Zhu S., Zhu Y., Santh T., Ranger S., Zhu Y., Shipe B., Spradling W., Studney W., Shong S., Zhu X., Shith H.O., Rang X.H., Zhong F.N., Woolage T., Worley C., Wu D., Yang S., Zhu X., Shith H.O., Ranger S., Zhu Y., Shith H.O., Ranger S., Zhu Y., Shith H.O., Ranger S., Zhu Y., Shith H.O., Shing X.H., Zhong F.N., Woolage C., Wu D., Yang S., Zhu X., Shith H.O., R
257 TVFRPVSETCTDRSGL--STGHWSGEVNDKNIQVVELPI-VDSLHPR-----PPYLPLAV 308
                                                    : : | : : | : | : | | : | 484 NKSKYIEELHQENKALKKKSSAESKQINAYEIKVNKLQLELESAKQKFQEMTDNYQKEIE 543
                                                                                                                                                                                                                                                                     544 VKKISEEKLLGEVEKAKAMVDEAVK-----LOKEIDLRCQHKIAEMVALMEKHKHQY 595
                                                                                                                                                                                                                                                                                                                                                                        DKVGTE-----DKKRVYLAT 408
                                                                                                                                                                                                                                                                                                                                                                                                                            PEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIE-EATKKLGFKHPVIGVHVRRT
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 41, Last sequence update) (Rel. 42, Last annotation update)
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MEDLINE=20196006; PubMed=10731132;
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QADFLVCTFSSQVCRVAYE----IMQTLHPDASANFHSLD---
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HSSP; P10587; 1BR.
InterPro; IPR000169; myosin_head.
InterPro; IPR000409; myosin_head.
InterPro; IPR004099; Myosin_N.
InterPro; IPR004091; Myosin_LillinerPro; IPR002017; Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain cortex;
MEDLINE=95301542; PubMed=7782316;
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Pfam; PF01576; Myosin_Lail; 1.
PRINTS; PR00193; MYOSINEAVY.
PVDDom; PD0000355; myosin_head; 1.
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
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Pfam; PF00063; myosin_head; 1.
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                                                                                  506 NQIAVYPHKPRTEE 519
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HHIALFDDKQMTKK 581
                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                              16-0CT-2001
                                                                                                                                                                                                                                      BOVIN
459
                                                                                                                          568
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                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 FDAALNALAEDVORVRETGHRLKNOVDTOYOOVENOTOVLGRLHDVSHLLRSAGT---- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KGCGYGCQL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TQM--QLVTGLQERNENQVVNALKIFMNFNTLEKSLDNLLATFIADMEQSLKECFAGNDI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 KTALEQINQFGYTSESSDQCIPQRFWQQVQQLLRKSFDECPQHVTQTLQEGLSKLLTSAR 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357 GLEQRLHGE-----FOFDNELFAP----LEVGYVSKCAANFKACLAGVDLPGNETVDN 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GTEAAFHPIEEYMVHV-----EEHFQLLAR-RMQVDKKRVYLATDDPTLL 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIRVASTELSAALIDSRLTNAIANVFAACGKELCTKLEAQIKLGADSKQV---VDLPNLQ 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEAKTKYSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHF-------LS 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
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                                                                           STRAIN=Berkeley; TISSUB=EMDATO;
MEDLINE=22426066; PubMed=12537569;
MEDLINE=22426066; PubMed=1253769;
MEDLINE=22426069; MEDLINE=2242609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 SVLNKSPTHNVSKPAPSRGPGKTPQLTTTQNFR--AKFWKSLHWLLYDELFETCTQIKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNDHPDHSS------RELSKILAKLERLKQQNEDLRRMAESLRIPEGP-IDQGTATGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 STG-----HWSGEVNDKNI-----QVVELPIVDSLHPRPPYLPLAVPEDLADRLL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase, FBgn0024689; fws. - Protein transport, Golgi stack;
Hypothetical protein; Transport; Protein transport, Golgi stack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        751 AA; 84953 MW; E32BID05BEEF6EBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 TELVQRRITYLQ--NPKDCSKARKLVCNIN-------
sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.9%; Score 120.5; DB 1;
20.7%; Pred. No. 1.1;
ive 97; Mismatches 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE003655; AAF53619.1; -. EMBL; AY069335; AAL39480.1; ALT_INIT.
                    Science 287:2185-2195(2000)
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Best Local Similarity 20.7%;
Matches 127; Conservative
                                                              SEQUENCE OF
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TICON K., Adelstein R.S.;

"Neuronal cell expression of inserted isoforms of vertebrate nonmuscle myosin heavy chain II-8."

"Neuronal cell expression of inserted isoforms of vertebrate nonmuscle myosin heavy chain II-8."

"Biol. Chem. 270:14533-14540(1995).

"I Biol. Chem. 270:14533-14540(1995).

"I FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS, CELL STAPRE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND CAPPING (BY SIMILARITY).

"I SUBJUIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CAPING SULATORY LIGHT CHAIN SUBDUITS (MLC. 2).

"I SUBJUITORY LIGHT CHAIN SUBDUITS (MLC. 2).

"I SUBJUITORY LIGHT CHAIN SUBDUITS (MLC. 2).

"I SUBJUIT OF A 28 - RESIDIUE REPRAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

"I STMILARITY: Contains I IQ domain.
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16-0CT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain,
type B) (Nonmuscle myosin heavy chain-B) (NMWHC-B).
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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"Bos taurus nonmuscle myosin heavy chain B mRNA, complete cds.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                 41 RELSKILAKLERLKQQNEDLRRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQ---- 96
                                                                                                                                                                1384 LGTIENL-EEAKKKLLKDVEVLSQRLEEKA----LAYDKLEKTK----TRLQQELDDLL
                                                                                                                                                                                        44; Indels 53; Gaps
                                                                                                                                                                              154 LDLGHHERSIMTDL-------YYLSQTDGA-GDWREKEAKDLT 188
                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                    "Human synaptonemal complex protein 1 (SCP1): isolation and characterization of the CDNA and chromosomal localization of the
                                                                                   Length 1976;
                              IQ.
COLLED COLL (POTENTIAL).
ATP (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL)
ALKYLATION (SH-2) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                     Meuwissen R.L.J., Meerts I., Hoovers J.M.N., Leschot N.J.,
                                                                     229097 MW; 6144354451C0F790 CRC64;
; 1.
Calmodulin-binding; Actin-binding;
                                                                                   3.9%; Score 119.5; DB 1; 25.7%; Pred. No. 4.5;
                                                                                                                                                                                                                                           Q15431; O14963;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Synaptonemal complex protein 1 (SCP-1 protein).
SYCP1 OR SCP1.
Homo sapiens (Human)
PROSITE; PS50096; IQ; 1.
Myosin; ATP-binding; Calmodulin-binding; Actin
Molad, ATP-binding; Calmodulin-binding; Actin
Mylad coll; Alkylation; Multigene family.
DOMAIN MYOSIN HEAD-LIKE.
                                                                                          ; Pred. No. 4.5; 33; Mismatches
                                                                                                                                                                                                                                     976 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Testis;
MEDLINE=98037449; PubMed=9371398;
                                                                            Query Match
Best Local Similarity 25./v.,
Best Local 5. Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch)
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COILED COIL (POTENTIAL).

NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

ARG/LYS-RICH (BASIC).

L -> F (IN REF. 2).

F -> Y (IN REF. 2).

F -> Y (IN REF. 2).

K -> T (IN REF. 2).

K -> D (IN REF. 2).

K -> D (IN REF. 2).

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E -> D (IN REF. 2).

E -> D (IN REF. 2).

ICHALITSEQYYSKEVKOLKTELENEK -> YSYCHYHKW TYLENEKGORPKLSSKRE (IN REF. 2).

LTSHCNKLSLENK -> YFTLQQASPPPN (IN REF. 2).

LTSHCNKLSLENK -> YFTLQQASPPPN (IN REF. 2).

LTSHCNKLSLENK -> YFTLQQASPPPN (IN REF. 2).

LTSHCNKLSLENK -> YFTLQASPPPN (IN REF. 2).
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FLANKED BY N- AND C-TERMINAL GLOBULAR DOMAINS. THE C-TERMINAL
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Pred. No. 2.1;
5; Mismatches 171; Indels 139;
                                                                                                                                                                                                                                       DR GO; GO:0005614; C:nucleus; TAS.

DR GO; GO:0005614; C:nucleus; TAS.

DR GO; GO:0005716; C:nucleus; TAS.

DR GO; GO:0007281; P:meiotic recombination; TAS.

DR GO; GO:0007283; P:mematogenesis; TAS.

TE DOMAIN 107 798 COILED COIL (PACIFIC)

FT DOMAIN 107 798 COILED COIL (PACIFIC)

FT DOMAIN 107 798 COILED COIL (PACIFIC)

FT DOMAIN 880 COILED COIL (PACIFIC)

TT DOMAIN 880 COILED COIL (PACIFIC)

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560 560 K -> T (IN REF. 2).

805 805 E -> D (IN REF. 2).

911 911 P -> S (IN REF. 2).

976 AA; 114069 MW; 8BA81D042AC2696B CRC64;
                                 DOMAIN HAS DNA-BINDING CAPACITY (BY SIMILARITY)
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363 MEESNKARARAHSFVVTEFE--TTVCSLEELLRTEQORLEKNEDQLKILTMELQKK----
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                                                                                                                                    PYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVIG
                                                                                                                                                                                                                                                                                                       362 VHVRRTDKVGTEAAFHPIEEYMVHVEEHF--QLLARRMQVDKKRVYL---ATDDPTLLKE
                                                                                                                                                                                                                                                                                                                                                                                      449 ENKQ-----FEKIAEELKGTEQELIGLLQAREKEVHDLEIQLTAITTSEQYYSKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D.-Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417 AK-----TKYSNYEFISD-NSISWSAGLHNRYTENSLRGVILDI 454
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Schizosaccharomycetales, Schizosaccharomycetaceae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O9UTK5; 013313; Q9UTT8;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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ALM1 OR SPAC1486.04C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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L219 SESVGERSNYLNMVALLNESNKSLRENLERNEERNITELREKIETLKTDLANFRLNKEQLE 1278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 --LQSELKKLKHLEGN--ELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGDWREKE-- 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 ---AKDLTELVQRRITYLQNPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRT 240
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"Large-scale screening of intracellular protein localization in living fission yeast cells by the use of a GFP-fusion genomic DNA library."; Genes Cells 5:169-180(2000).
-!- FUNCTION: AFTER THE ONSET OF MITOSIS, AT MID- TO LATE ANAPHASE, CO-LOCALIZES WITH THE MEDIAL ACTIN RING. MAY PLAY A ROLE IN
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                                                                                                                                                                                                  SUBCELLULAR LOCATION: Cytoplasmic.
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EMBL; AF010473; AANGS416.1; ALT_INIT.
EMBL; ABC02012; BAANG7316.1; -.
PIR; T50073; T50073.
GeneDB_SPombe; SPAC1486.04c; -.
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1727 AA; 197858
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 PYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKL--GFKHPV 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 PKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILES-------QN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           947 MLEEAKHRETV--LREEATEWEEKHDII-----SNESLKLRNEIERIRSDAEEDIQK 996
                                                                                                                                                                                                                                                                                                          RELSKILAKLERLKOO-----NEDLRRMAESLR--IPEGPIDOGTATGRVRVLEEQLVKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80; Mismatches 181; Indels 124; Gaps
                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoldea;
Ascarididae; Parascaris.
NCBI_TaxID=6257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 1955;
                              061308;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
227 KDa spindle- and centromere-associated protein (PUMA1).
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COLLED COLL (POTENTIAL).

227216 MW, 495B8F92A5C0A111 CRC64,
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitosis; Meiosis; Centromere;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94; Conservative
                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317
1747
1813
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                      PUMA PARUN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
PUMA_PARUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                         DATA BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE B
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                                              360 IGVHVRRTDKVGTEAAFHPIEEYMVHVEEHFOLLARRMQVDKKRVYLATDDPTLLKEAKT 419
                                                                                                                                                                                              50 LERLKQONEDLRRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIENYKKQARNGLG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       crenarchaeon, Aeropyrum pernix Kl.";

DNA Res. 6:83-101(1999)

-!- FUNCTION: Involved in DNA double-strand break repair (DSBR). The rad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mrell by unwinding
                                                                                                                                                       KYSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kosugi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome. NP BIND 31 38 ATP (BY SIMILARITY). DOWAIN 202 758 COILED COIL (POTENTIAL). SEQUENCE 919 AA, 104138 MW; 7BF4A80EB601B9DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and/or repositioning DNA ends into the mrell active site (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.8%; Score 116.5; DB 1; Length 919;
22.5%; Pred. No. 2.6;
iive 70; Mismatches 160; Indels 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99110339; PubMed=10382966; MEALARABASARI S., Haikawa Y., Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosug Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; "Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
-!- SUBUNIT: Forms a complex with mrell (By similarity).
-!- SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aeropyrum pernix.
Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
Desulfurococcaceae; Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA double-strand break repair rad50 ATPase.
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PIR, B72765; B72765.
HAMAP, MF 00449; -; I.
InterPro; IPR003499; ABC transporter.
InterPro; IPR003405; SMC_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPRO03395; SMC_C.
Pfam; PF04423; Rad50_zn_hook; 1.
Pfam; PF02483; SMC_C; 1.
Pfam; PF02483; SMC_C; 1.
Dfam; PF02463; SMC_N; 1.
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522 LSRLNQLEEGLREL--GFQTPE---DLAKAEQKLRMLRERLEELRKLENSLEEKVRN-LS 575
                        ---RRI---ENGAKELWFFLOSELKKLKHLEGNELORHADEILLDL 156
                                                                        GHHERSIMTDLY----YLSQTD---GAGDWREKEAKDL------TELVQRRITYL 198
                                                                                                                                                                        258 VFRPVSETCTDRSGLSTGHWSGEVNDKNIQVVELPIVDSLHPRPPYLPLA----VPEDLA 313
                                                                                                                                                                                                                         D----RLLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVIGVHVR---- 365
                                                                                                                                                                                                                                                                        ---RIDKVGTEAAFHPIEEYMVHVEEHFQL----LARRMQVDKKRVYLATDDPTLLKEA 417
                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MUSCLE CONTRACTION.
-!- SUBDUNT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
-!- SUBDUNT: MUSCLE MYOSIN IS A HEXAMERIC LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.
-!- FTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
-!- MISCELLANGOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) IT CAN LATER BE
                                                                                                                                                                                                 IDREMGELQTRIREMKSRKASGE-----EALKL-----YLPAAASRRIMEEIG
                                                                                                                                                                                                                                                 :: || :: | |:: | |:: | |:: | |:: | |:: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: |
                                                                                      REIEVKAIGGNGAYRPLE--AVSGGERTVLALSFVLALNKAVGGKLGFLALDEPTANLDE
                                                                                                                                                                                                                                                                                                                          418 KTKYSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADF--LVC--TFSSQVCR
                                                                                                                        ONPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLI-LESQNWRYATGGWET
                                                                                                                                              E-----QNTLAELDDRISR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=BISTEOL N.2.
MEDLINE=89178677; PubMed=2926820;
Dibb N.J., Maruyama I.N., Krause M., Karn J.;
Sequence analysis of the complete Caenorhabditis elegans myosin heavy chain gene family.";
Now No. 1. 8101. 205:603-613(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P12844; Q21440;
01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
28-FES-2003 (Rel. 41, Last annotation update)
MYO-3 OR K12F2.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                        KDHEILR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1039 KLEQQMDEL-----EENID------EGD 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 CSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQNWRYATGGWETVFRPVS 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETCTDRSGLSTGHWSGEVNDKNIQVVELP-IVDSLHPRPPYLPLAVPEDL-ADRLLRVHG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----R 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGDWREKEAKDLTELVQRRITYLQNPKD
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                                                                                       BODY
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> YVRKLKLFKKKINTIQKLNRLNFQ (IN REF.
                                                                                MISCELLANBOUS: MHC A AND MHC B ARE FOUND EXCLUSIVELY IN THE WALL MUSCLE. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAMENT. SIMILARITY: Contains 1 myosin-like globular head domain. SIMILARITY: Contains 1 IQ domain.
                                             DIFFERENT MYOSIN HEAVY CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 116.5; DB 1; Length 1969;
Pred. No. 7.1;
69; Mismatches 148; Indels 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.
ATP.
ACTIN-BINDING.
ACTIN-BINDING.
ACTIN-BINDING.
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMAKI; SHOWALL, SHOWALL, SMAKI; SHOWSIN; PROSIN; PROSIN; PROSIN; Macle protein; Coiled coil; Thick filament; AC MYP-binding; Methylation; Alkylation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVIGVHV---
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HORMPEP): KLZPZ.1, C312204.
HOTERPEO; IPR000048; IQ_region.
HOTERPEO; IPR001609; Myosin_No.
HOTERPEO; IPR001609; Myosin_No.
HOTERPEO; IPR002928; Myosin_Lail.
Pfam; PF01676; Myosin_Lail.
Pfam; PF01576; Myosin_Lail; 1.
ProDom; PD000355; Myosin_Lail; 1.
SWART; SM00115; IQ; 1.
SWART; SM00115; IQ; 1.
                                             MISCELLANEOUS: THERE ARE FOUR C.ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.8%;
19.1%;
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X08067; CAA30356.1; -.
EMBL; Z78199; CAB01576.1; -.
PIR; T23622; S02771.
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GO:0006899; P:non-selective vesicle transport; TAS
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Matches
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     366 RTDKVGTEAAFHPIE----EYMVHVEEHFQLLAR-------RMQVDKKRVYLATDDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: SEEMS TO BE A INTERMEDIATE FILAMENT ASSOCIATED PROTEIN THAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISOIG=P30622-2; Sequence=VSP 000765;
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE REED-STERNBERG CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Peripheral blood monocytes;
MEDLINE=92289675; PubMed=1600942;
Bilbe G., Delable J., Brueggen J., Richener H., Asselbergs F.A.M.,
Cerletti N., Sorg C., Odink K., Tarcsay L., Wiesendanger W.,
de Wolf-Peeters C., Shipman R.;
"Restin: a novel intermediate filament-associated protein highly
expressed in the Reed-Sternberg cells of Hodgkin's disease.";
EMBO J. 11:2103-2113(1992).
                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last Sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
Restin (Cytoplasmic linker protein-170 alpha-2) (CLIP-170) (Reed-Sternberg intermediate filament associated protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                               446
                                                                                                                                                                              T-----LLKEAKTKYSNYEFISD---NSISWSAGLHNRY-TENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92405160; PubMed=1356075;
Pierre P., Scheel J., Rickard J.B., Kreis T.E.;
"CLIP-170 links endocytic vesicles to microtubules.";
Cell 70:887-900(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0005882; C:intermediate filament; TAS.
GO:0015630; C:microtubule cytoskeleton; TAS.
GO:0008017; F:microtubule binding activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                        1427 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF HODGKIN'S DISEASE. SIMILARITY: Contains 2 CAP-Gly domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P30622-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO:0005768; C:endosome; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X64838; CAA460S0.1; -.
EMBL; M97501; AAA35693.1; -.
PIR; S22695; S22695.
Genew; HGNC:10461; RSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -! - ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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963 FLQKSIEDMTVKAEQSQQEAAKKHEBEFKKELERKLSD--LEKKMETSHNQCQELKARYER 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        431 SISWSAGLHNRY-----TENSLR-----GVILDIHFL-SQADFLVCTFSSQVC 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 YYLSQTDGAGDWREKEAKDLTELVQRRITYLQNPK--DCSKARKL-----VCNIN 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 KGCGYGCQLHHVVYCFMIAYGTQRTLILESQNWRYATGGWETVFRPVSETCTDRSGLSTG 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F--HPIEEYMVHVEEHFQLLARRMQVDKKRVYLATDDPTLLKEAKTKYSNYEFIS---DN 430
                                                                                                                                                                                                                                                                                                                                                                                                                                           84
                                                                                                                    Cytoskeleton, Microtubules, Coiled coil; Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                         40 SRELSKILAKLERLKQQNEDL------RRMAESLRIPEGPIDQGTATGRVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 VLEEQLVKAK-----EQIENYKKQARNGLGKDHEILRRRIENGAKELWFFLQS----
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                                                                                                                                                                                                                                                                                                                                                                3.7%; Score 115.5; DB 1; Length 1427;
17.9%; Pred. No. 5.5;
tive 97; Mismatches 208; Indels 157;
                                                                                                                                                                                                                                                                             -> E (IN REF. 2).
0A4F166DD94254E8 CRC64;
                                                                                                                                                                                                                                                                 Missing (in isoform Short). / FTId=VSP_000765.
                                                                                                                                                                                                                       COILED COIL (POTENTIAL).
CCHC-BOX.
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Last annotation update)
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                                                                                                                                             CAP-GLY 1.
SER-RICH.
                                                                                                                                                                                CAP-GLY 2.
SER-RICH.
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1078 EDAMQIMEQMTKEKTETLASLED 1100
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InterPro; IPR000938; CAP-Gly.
InterPro; IPR001878; Znf CCHC.
Pfam; PF01302; CAP-GLY; Z.
SMART; SM00343; ZnF C2HC; I.
PROSITE; PS00845; CAP-GLY 1; Z.
PROSITE; PS50245; CAP-GLY 2; Z.
                                                                                                                                                                                                                                                                                                        1069 1069 D -:
1427 AA; 160989 MW;
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16-0CT-2001 (Rel. 40, Last seque
16-0CT-2001 (Rel. 40, Last annot
0steoclast stimulating factor 1.
OSTF1.
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Q92882;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.7%; Score 114; DB 1; Length 214;
Best Local Similarity 38.0%; Pred. No. 0.57;
Matches 27; Conservative 12; Mismatches 22; Indels 10; Gaps
                                                                                                                                                             Reddy S.V., Devlin R., Menaa C., Nishimura R., Choi S.J., Dallas M., Yoneda T., Roodman G.D.;
"Isolation and characterization of a cDNA clone encoding a novel peptide (OSF) that enhances osteoclast formation and bone
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                        71 SH3.
101 ANK 1.
135 ANK 3.
1168 ANK 3.
23799 MW; E10C6570B68E3D6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew, HGNC:8510, OSTF1.

GO; GO:0005622; C:intracellular; TAS.

GO; GO:0005515; F:protein binding activity; TAS.

GO:00005515; P:protein binding activity; TAS.

GO; GO:0001503; P:ossification; TAS.

GO; GO:0007165; P:signal transduction; TAS.
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SH3 domain; Repeat; ANK repeat.
11 PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00248; ANK; 2.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
PROSITE; PS50297; ANK REP RECION; 1.
PROSITE; PS50088; ANK_REPEAT; 1.
                                                                                                                                                                                                                                                                             Cell. Physiol. 177:636-645(1998)
                                                                                                    SEQUENCE FROM N.A.
TISSUE=Bone marrow;
MEDLINE=99190637; PubMed=10092216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U63717; AAB06396.1; -. HSSP; P06241; 1SHF.
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Pfam; PF00018; SH3; 1.
PRINTS; PR00452; SH3DOMAIN.
ProDom; PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nterPro; IPR002110; ANK.
interPro; IPR001452; SH3.
sapiens (Human)
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                                                               _TaxID=9606;
                                                                                                                                                                                                                                                         resorption.";
                                                                                                                                                                                                                                                                                                                      SMN1 BINDING.
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565 VKYPTYPEAEK 575 : | : | :: 73 IDNPLHEAAKR 83

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February 2, 2004, 08:39:43 ; Search time 33.5 Seconds (without alignments) 4429.261 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                  OM protein - protein search, using sw model
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sp_unclassified:*
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sp_archeriap:*
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	QBaxs7 xenopus lae QBnep2 homo sapien Q9vyv5 d putative O16882 caenorhabdi Q8iua5 homo sapten Q8ifw9 ciona intes Q8ifw9 ciona intes Q8ifw8 ciona intes Q8ifw8 ciona intes Q8ifw8 ciona intes Q8ifw8 ciona intes Q8ifw8 ciona intes Q8ifw8 ciona intes Q8ifw8 ciona intes Q8ifw8 ciona intes Q8ifw9 leptospira Q8ifw8 leptospira Q9sax5 ratius norv Q9sax5 ratius norv Q9usm2 plasmodium Q8vrog thermoanaer Q8bul8 mus musculu
SUMMARIES	QBAXS7 QBNEP2 QBVVVS QQ9VVVS O16882 QBIVM9 QBIFW9 QBIFW9 QBIFW2 QBIED2 QBIED2 QBIED2 QBIED2 QBIED2 QBIED2 QBIED2 QBIED2 QBIED2 QBIED2 QBIED2 QBIEM2 QBIEM2 QBIEM2
DB	113 114 117 110 110 110 110 110
% Query Match Length DB	578 446 619 559 169 560 1113 1218 876 1025 745 462 35462 35462
% Query Match	0.084 0.012 0.012 0.014 0.054 0.056 0.
Score	2830.5 1480.5 1480.5 978 810 670 670 129.5 129.5 120 120 120 120 120 120 120 120 120 120
Result No.	11111111111111111111111111111111111111

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Q921B9 Q8B3M2 Q96YQ6 Q9SA62 Q9SA62	Q9H2G7 Q8TC31 Q98TQ5 Q18106 Q9UEG2 Q9V5J0	0956V1 093250 066878 09LP90 096JV2 08INU2	Q9UFE4 Q9UFE4 Q93155 Q93155 O61639 O76571 Q19658 Q22869 Q96ED9
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RADAMS M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

RADE GOCGE R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RADE GOCGE R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RADE Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RADAMS M. Basu A., An H.-J., Andrews-Péannocch C.R., Miklos G.L.G.,

RADE BALLON R.M., Basu A., Baxendale J., Bhandari D., Bolshakov S.,

RADE BALLON R.M., Basu A., Baxendale J., Brandari D., Bolshakov S.,

RADE BORKOVA. B. Botcher H., Bouck J., Broweren P., Brotter P., Chamdra I.,

Burtis K.C., Busam D.A., Buller C., Davenport L.B., Davies P.,

RADE Pablos B., Delcher A., Dong Z., Mays A.D., Dew I., Diterz S.M.,

RADORD K., Doug L.B., Downes M., Dugan-Rocha S., Dunkov B.C.,

Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann M.,

RADORD K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Alock A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RADISH B.E., Kodira C.D., Kraft C., Kravitz S., Kulb D., Lai Z.,

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RADISH B.E., Kodira C.D., Kraft C., Kravitz S., Kulb D.,

RADISH B.E., Kodira C.D., Kraft C., Kravitz S., Kulb D.,

RADISH B.E., Kodira C.
                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEWBLrel. 13, Last sequence update)
01-MAR-2003 (TrEWBLrel. 23, Last annotation update)
Putative alpha-(1,6)-fucosyltransferase (BC 2.4.1.68) (Glycoprotein 6-
alpha-L-fucosyltransferase) (GDP-fucose--glycoprotein
fucosyltransferase) (GDP-L-Puc:N-acetyl-beta-D-glucosaminide alphal,6-
                                                 KKRVYLATDDPSLLKEAKTKYPNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQA
                                                                                                                     Petit D., Picaud F., Dupuy F., Germot A., Julien R., Maftah A.; "Core al- and a6-fucosyltransferases in Drosophila: characterization and origin of diversity."

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                       IPMEPGDIIGVAGNHWDGYSKGINRKLGKTGLYPSYKVREKIETVKYPTYPEAEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                              Created)
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SEQUENCE FROM N.A.
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AIENGAKEFWYLVQSEVKKLKHLDRNELQRHVDEILIDMGHQQRSVMTDLYYLSQTDGAG 180
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                                                                                                                                                 GCQLHHVVYCFMIAYGTQRTLILESQNWRYATGGWETVFRPVSETCTDRSGISTGHWSGE
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                                                                                                                                                                                                                                                                                                                   GCQLHHVVYCFMIAYGTQRTLILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGE
                                                                                                                           QRILILESQNWRYATGGWETVFRPVSETCTDRSGLSTGHWSGEVNDKNIQVVELPIVDSL
                                                                                                                                                                                                             HPRPPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKH
                                                                                                                                                                                                                                                                                                PVIGVHVRRTDKVGTEAAFHPIEEYMVHVEEHFQLLARRMQVDKKRVYLATDDPTLLKEA
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hymochetical protein.
Homo sapiens (Human).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE-Testis;
Strausberg R.;
Strausberg (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51138 MW; 89DAC51B0B7C57FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYSKGINRKLGKTGLYPSYKVREKIETVKYPTYPEAEK
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InterPro; IRR001452; SH3.
SMART; SM00326; SH3; 1.
Hypothetical protein.
SEQUENCE 446 AA; 51138 MW
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Matches 399; Conservative
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Q8NEP2;
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MEDLINE=99069613; FubMed=9851916;
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Submitted (DEC-2002)
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SEQUENCE FROM N.A.
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C10F3.6 OR FUT8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTALYTIC ACTIVITY: GDP-L-FUCOSE + N4-(N-ACETYL-BETA-D-GLUCOSAMINYL-1, 2-ALPHA-D-MANNOSYL-1, 3-(R(1)-ALPHA-1, 6)-BETA-D-MANNOSYL-1, 3-(R(1)-ALPHA-1, 6)-BETA-D-MANNOSYL-1, 4-D-GLUCOSAMINYL-1, 4-N-ACETYL-D-GLUCOSAMINYL)ASPARAGINE = GDP + N4-(N-ACETYL-BETA-D-GLUCOSAMINYL-1, 2-ALPHA-D-MANNOSYL-1, 3-(R(1)-ALPHA-1, 6)-BETA-D-MANNOSYL-1, 4-BETA-D-MANNOSYL-1, 6)-BETA-D-MANNOSYL-1, 6)-BETA-D-MANNOSYL-1, 6)-N-ACETYL-D-GLUCOSAMINYL-D-GLUCOSAMINYL-1, 4-(ALPHA-L-FUCOSYL-1, 6)-N-ACETYL-D-GLUCOSAMINYL)ASPARAGINE.
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SMART; SM00326; SH3; 1.
Hypothetical protein; Transferase; Glycosyltransferase; Transmembrane;
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1 17 CYTOPLASMIC (POTENTIAL).

8 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMPORTANT FOR DONOR SUBSTRATE BINDING (BY SIMILARITY).
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                                                                                                                                                         STRAIN=Berkeley; TISSUB=Testis; Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K. Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
          Yao Q.A.,
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Williams S.W., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";
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LUMENAL, CATALYTIC (POTENTIAL)
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Best Local Similarity 46.5%; Pred. No. 3.7e-102;
Matches 285; Conservative 108; Mismatches 169;
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EMBL; AE003487; AAF48079.1; --
EMBL; AY051461; AAK92875.1; --
Flyase; Flyase; CG2448.
Interpro; IPR001452; SH3.
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                                                                                                                                                  RVHGDPAVMWVSQFVKYLIRPQPWLEKEIEEATKKLGFKHPVIGVHVRRTDKVGTEAAFH
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LONPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQRTLILESQNWRYATGGWET
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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Martinez-Duncker I., Mollicone R.;
"Cloning, expression and genomic organization of two core
fucosyltransferases (CEE and CED) from Caenorhabditis elegans.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF022968; AAN84870.1; -.
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01-WAR-2003 (TrEMBirel. 23, Last annotation update)
Hypothetical protein C10F3.6 (Core alpha-6-fucosyltransferase)
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STRAIN=Bristol N2;
Davidson S., Wohldmann P.;
"The sequence of C. elegans cosmid ClOF3.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
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AJ514325; CAD55805.1;
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                                                                    Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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TISSUB-Embryo,

MEDLINE=22326102; PubMed=12438718;

Coullin P., Crooijmans R.P.M.A., Groenen M.A.M., Heilig R.,

Mollicone R., Oxiol R., Candelier J.J.;

"Assignment of FTTB gene to chicken chromosome band 5q1.4 and to lchromosome 14q23.2-24.1 by in situ hybridization. Conserved and compared synteny between human and chicken.";

Cytogenet. Genome Res. 97:234-238 (2002).

EMBL; AJ514224; CAD55804.1;
                                                                    50;
                                             Length 559;
                                           Query Match
31.7%; Score 978; DB 5; Length 55
Best Local Similarity 36.8%; Pred. No. 1.2e-64;
Matches 211; Conservative 121; Mismatches 191; Indels
 EMBL, AJ512486, CAD54736.1, -.
Hypothetical protein; Glycosyltransferase, Transferase.
SEQUENCE 559 AA; 63648 MW; BBF6F1944A9BEF9F CRC64;
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Last sequence update)
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                                                                                                                                                                                                                                                                                         KYSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLSQADFLVCTFSSQVCRVAYEIM
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Phlebobranchia; Cionidae; Ciona.
NCBI_TaxID=7719;
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30.1%; Pred. No. 1.2e-41;
ive 90; Mismatches 204; Indels
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19520 MW; 0ACD43AA0F56AB31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        575
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94.2%; Pred. No. 8.3e-53;
ive 6; Mismatches 3.
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Best Local Similarity 30.1%
Matches 157; Conservative
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169 AA;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Mollicone R., Michalski J.C., Bauvy C., Cailleau-Thomas A.,
Mollicone R., Martinez-Duncker I., Breton C., Codogno P., Oriol R.;
Candelier J.J., Martinez-Duncker I., Breton C., Codogno P., Oriol R.;
Splice variants of alpha-6-fucosyltransferase are expressed early in
human embryogenesis.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ518152; CAD56162.1;
Transferase; Glycosyltransferase.
Transferase; Glycosyltransferase.
Transferase; Glycosyltransferase.
                                                           196 MSNLAYP--NMDKIFLPLSRTCLTAEGNVDDYPEWESP-NDEHPSSSDAPIVKVSIVYRR
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              STSHADTSSRLSSDGLKGIVTDVHLLVECDHFVGTFSSNIGRLVYEMKQQYGSDPTFTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 HPRPPYLPLAVPEDLADRILLRVHGDPAVWWVSQFVKYLIRPQPWLEKEIEEATKKLGFKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 QLKITYPKYRIVQIQKNAV---VALAKRFSGSGLEGILQDVFLMAECDYFVGTMSSNVGR
                                               ---RTEEEIPMEPGDIIG
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Phlebobranchia; Cionidae; Ciona.
NCBI_TaxID=7719;
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                                                                                           VAGNHWDGY-SKGINRKLGKTGLYPSYKVREKIETVKYPTY 570
                                                                                                         01-WAR-2003 (TrEMBLrel. 23, Last sequence update) 01-WAR-2003 (TrEMBLrel. 23, Last annotation update) Putative alpha-6-fucosyltransferase (EC 2.4.1.68).
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                                               HSLDDIYYFGGQNAHNQIAVYPHKP--
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Best Local Similarity 32.94
Matches 140; Conservative
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Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
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20.7%; Pred. No. 0.79;
ive 96; Mismatches 156;
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SEQUENCE 876 AA;
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SEQUENCE FROM N.A.
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C STRAIN=AV19 / DSM 6324 / JCM 9639;
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Archaea; Buryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
  Harris B., Lennard N., Clark L., Line A., Barron A., Corton C., Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL644509; CAD52328.1; -. SEQUENCE 1218 AA; 143059 WW; EIDBD7838BBC7E5B CRC64;
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876 AA; 103706
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Matches 100; Conservative
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InterPro, IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 11.
SMRAT; SM01085; ARN; 8.
PROSITE; PS0176; ARM REPEAT; 7.
SEQUENCE 745 AA; 81777 MW; 9E
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                     Gaps
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STRAIN=Sprague-Dawley; TISSUE=Vagina;
Umekita Y., Liao S.;
"Molecular cloning and sequencing of the rat plakoglobin cDNA.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                     84; Mismatches 207; Indels 204;
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         EMBL; AC007296; AAD30251.1; -.
SEQUENCE 1025 AA; 116411 MW; 08C952A2032BA1E4 CRC64;
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Hilpakka R.A.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; USB8S8; AABO6317.1;
HSSP; Q02248; 2BCT.
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Last annotation update)
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Pred. No. 1.8;
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                                                                                                                                                                                                                                                                                                                                                                                   81 GRVRVL------EEQLVKAKEQIENYKKQARNGLGKDH--EILRRRIENGAKEL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                         WFFLOSELKKLKHLEGNEL----ORHADEILLDLGH-----HERSIMTDLYYLSQTDG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 -GKFLEKE----KELINKLRVYAEDIKDDSSVLFLSIMNKNK-------KNL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YGTQRTLILESQNWRYATGGWETVF--RPVS------ETCTDRSGLSTGHWSGE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 VNDKNIQVVELPIVDSLHPRPPYLPLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQP 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 WLEKEIEEATKKLGFKHPVIGVHVRRTDKVGTEAAFHPIEEYMVHVEEHFQLLARRMQV- 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -KEKDIE----KIAF----IMRSNK-----DFFILNIDNNONLTCKTIHFS 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -DKKRVYLATDDPTLLKEAKTKYSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHFLS 458
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                                                                                                                                                                                                                                                                                                                           29 LVRDN------DHPDHSSRELSKILAKLERLKQQNEDLRRMAESLRIPEGPIDQGTAT 80
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                                                                              MEDLINE=21886394; PubMed=11889109; Rapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A Bhattacharrya A., Bartman A., Gardher W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman B., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R.; "Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 2588 ["].

"Bacteriol. 184:2005-2018 [2002].

EMBL; AE010464; AAL93679.1; --.
                                                                                                                                                                                                                                                                     3.9%; Score 121; DB 16; Length 462; 18.1%; Pred. No. 1.2;
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 Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                           462 AA; 54390 MW; 5D661B65C146377A CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2003 (TrEMBLrel. 23, Last annotation update)
FCR3 CSA ligand (Fragment).
                                                                                                                                                                                                                                                                                                94; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 18.1%
Matches 106; Conservative
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                                                                       25586;
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                             NCBI_TaxID=76856;
                Fusobacterium
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1308 PPR----ROKLCVHFLANDNEIKKLOSQVNLKBAFIKSAAABTFFSWYYKKS----KDGE 1359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----WFFLQSELKKLKHLE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 GNELQRHADEILLDLGHHERSIMTDLYYLSQTDGAGDWREKEAKDLTELVQRRITYLQNP 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HVRRTDKVGTEAAFHPIEEYMVH------VEEHFQLLARRMQVDKKR-----VYLA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLAVPEDLADRLLRVHGDPAVWWVSQFVKYLIRPQPWL--EKEIEEATKKLGFKHPVIGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 DHPDHSSRELSKILAKLERLKQQNEDLRRMAESLRIPEGPIDQGTATGRVRVLEEQLVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259 FRPVSETCTDRSGLST--GHWSGEVNDKNIQVVELP------IVDSLHPRPPYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         408 TDD------PTLLKEAKTKYSNYEFISDNSISWSAGLHNRYTENSLRGVILDIHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buffet P., Gamain B., Scheidig C., Baruch B., Oishi S., Fujii N. Fusai T., Parzy D., Miller L.H., Gysin J., Scherf A.; Fusai T., Parzy D., Miller L.H., Gysin J., Scherf A.; Plasmodium falciparum domain mediating adhesion to chondroitin sulfate A: A receptor for human placental infection."; Proc. Natl. Acad. Sci. U.S.A. 96:12743-12748(1999).

EMBL; AJ13811; CAB59840.1; -.

InterPro; IPR004258; PEMP.

Pfam; PF03011; PFMP.

NON_TER 3542
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Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                    3542 AA; 413089 MW; 970D85EE88DA2EC2 CRC64;
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 KEQIENYKKQARNGLGKDHEILRRRIENGAKEL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203;
                                                                                                                                                                                                                                                                                                                                                                                                                                 3.9%; Score 120.5;
19.1%; Pred. No. 22;
ive 94; Mismatches
                                                                                                    STRAIN=FCR3;
MEDLINE=20006305; PubMed=10535993;
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01-MAR-2003 (TEEMBLrel. 23, La
ATPase involved in DNA repair.
SECC OR TTE0266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                         SEQUENCE FROM N.A.
                       NCBI_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 KVGTEAAFHPIEEYMVHVEEHFQLLARRMQVDKKRVYLATDDPTLLKEAKTKYSNYEFIS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                            49 KLERLKQQNEDLRRMAESLRIPEGPIDQGTATGRVRVLEEQLVKAKEQIENYKKQARNGL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 GKDHEILRRRIENGAKELWFF-------LOSELKKL-KHLEGNELQRHA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 DEILLDL-----GHHERSIM----TDLYYLSQTDGAGDWREKEAKDLTELVQ 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 TGGWETVFRPVSETCTDRSGLSTGHWSGEVNDKNIQVVELPIVDSLHPRPPYLPLAVPED 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   939 ---NIERLEG------FLKGROIEEEHWNRLEERIRELEEILTGKRKEIG----- 979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 RRITYLONPKDCSKARKLVCNINKGCGYGCQLHHVVYCFMIAYGTQR-TLILESQNWRYA 251
                                                                                                                                                                                                                                                                                                                                                        Query Match 3.9%; Score 120; DB 16; Length 1177; Best Local Similarity 19.9%; Pred. No. 5.1; Matches 99; Conservative 83; Mismatches 166; Indels 150; Gaps
                                                                                            SEQUENCE FORM N.A.

SEQUENCE FORM N.A.

MEDLINE=21992816; PubMed=11997336;

Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,

Tan H., Chen R., Wang H.;

"A complete sequence of T. tengcongensis genome.";

Genome Res. 12:689-700(2002).

EMBL; AE012999; AAM23562.1; -.

InterPro; IPR003439; ABC_transporter.

Complete proteome.

SEQUENCE 1177 AA; 138340 MW; D53567E10E127983 CRC64;
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
                 Thermoanaerobacteriaceae; Thermoanaerobacter.
NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1027 -----
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